

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 860 Seconds  
(without alignments)  
6955.045 Million cell updates/sec

Title: US-09-645-590-1

Perfect score: 138

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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# ALIGNMENTS

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LOCUS AR176719 Sequence 5 from patent US 6312898.
DEFINITION AR176719 Sequence 5 from patent US 6312898.
ACCESSION AR176719
VERSION AR176719.1 GI:17919074
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 551)
AUTHORS Koulu,M., Karvonen,M., Pesonen,U. and Uusitupa,M.
TITLE Diagnosis of a person's risk of developing atherosclerosis or
diabetic retinopathy based on leucine 7 to proline 7 polymorphism
in the prepro-neuropeptide Y gene

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	138	100.0	551	6	AX138816	Sequence
3	138	100.0	551	6	AX139001	Sequence
4	138	100.0	551	6	AX139420	Sequence
5	138	100.0	551	6	AX337554	Sequence
6	138	100.0	551	6	AX463054	Sequence
7	138	100.0	551	6	BD015786	Compound
8	138	100.0	551	6	BD015859	Compound
9	138	100.0	551	6	BD103561	Variant p
10	138	100.0	551	9	HUMNPY	Human neuro
11	138	100.0	551	11	GI8330	sWS51475 Er
12	138	100.0	568	9	BC029497	Homo sapi
13	113.2	82.0	122	6	AR416737	Sequence
14	113.2	82.0	122	6	BD112290	EST and e
15	91	65.9	325	6	AR176715	Sequence
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22	84.2	61.0	169	6	BD033296	Sequence
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24	65.4	47.4	452	4	OAR417904	Ovis arie
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27	63.2	45.8	707	6	AX525587	Sequence
28	63	45.7	483	6	AX305379	Sequence
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35	49	35.5	130	6	BD033295	Sequence
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LOCUS 551 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 8 from Patent EP1097706.
ACCESSION AX138816
VERSION AX138816.1 GI:14274563
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Maw,G.N. and Wayman,C.P.
TITLE Phosphodiesterase inhibitors for the treatment of female sexual
dysfunction
JOURNAL Patent: EP 1097706-A 8 09-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
FEATURES Location/Qualifiers
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QY 121 TGACCCCTGCCCTGTGCC 138
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RESULT 3
AX139001
LOCUS 551 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 8 from Patent EP1097707.
ACCESSION AX139001
VERSION AX139001.1 GI:14274691
KEYWORDS
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Maw,G.N. and Wayman,C.P.
TITLE Treatment of female sexual dysfunction
JOURNAL Patent: EP 1097707-A 8 09-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
FEATURES Location/Qualifiers
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AX139420
LOCUS 551 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 8 from Patent EP1097719.
ACCESSION AX139420
VERSION AX139420.1 GI:14275073
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Maw,G.N. and Wayman,C.P.
TITLE Nep inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
FEATURES Location/Qualifiers
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Db 121 TGACCCCTGCCCTGTGCC 138

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AX337554  
LOCUS AX337554 551 bp DNA linear PAT 09-JAN-2002  
DEFINITION Sequence 8063 from Patent WO0194629.  
ACCESSION AX337554  
VERSION AX337554.1 GI:18128273  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Horrigan, S., Soppet, D.R. and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 8063 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
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AX463054  
LOCUS AX463054 551 bp DNA linear PAT 15-JUL-2002  
DEFINITION Sequence 1 from Patent WO0247670.  
ACCESSION AX463054  
VERSION AX463054.1 GI:21886069  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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REFERENCE  
AUTHORS Naylor, A.M., van der Graaf, P.H. and Wayman, C.P.  
TITLE Treatment of male sexual dysfunction  
JOURNAL Patent: WO 0247670-A 1 20-JUN-2002;  
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DB 121 TGACCCCTCGCCCTGTGCC 138  
RESULT 7  
BD015786  
LOCUS BD015786 551 bp DNA linear PAT 27-AUG-2002  
DEFINITION Compound for treatment of female sexual dysfunction.  
ACCESSION BD015786  
VERSION BD015786.1 GI:22556923  
KEYWORDS JP 2001206855-A/4.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 551)  
REFERENCE  
AUTHORS Maw, G.N. and Wayman, C.P.  
TITLE Compound for treatment of female sexual dysfunction  
JOURNAL Patent: JP 2001206855-A 4 31-JUL-2001;  
PFIZER INC  
COMMENT  
OS Homo sapiens (human)  
PN JP 2001206855-A/4  
PD 31-JUL-2001  
PR 08-NOV-2000 JP 2000339905  
PR 08-NOV-1999 GB 9926437.6, 18-FEB-2000 GB 0004021.2 PR  
26-MAY-2000 GB 0013001.3, 05-JUL-2000 GB 0016563.9 PR  
12-JUL-2000 GB 0017141.3  
PI GRAHAM NIGEL MAW, CHRISTOPHER PETER WAYMAN  
PC A61K45/00, A61K31/122, A61K31/165, A61K31/17, A61K31/18, A61K31/19,  
PC A61K31/191,  
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DEFINITION    Compound for treatment of female sexual dysfunction.
ACCESSION    BD015859
VERSION      BD015859.1 GI:22556996
KEYWORDS     JP 2001213802-A/4.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 551)
REFERENCE    Maw,G.N. and Wayman,C.P.
AUTHORS     Compound for treatment of female sexual dysfunction
TITLE       PFIZER INC
JOURNAL
COMMENT
OS          Homo sapiens (human)
PN          JP 2001213802-A/4
PD          07-AUG-2001
PR          08-NOV-2000 JP 2000339853
PR          08-NOV-1999 GB 9926437.6,18-FEB-2000 GB 0004021.2 PR
26-MAY-2000 GB 0013001.3,05-JUL-2000 GB 0016563.9 PR
12-JUL-2000 GB 0017141.3
PI          GRAHAM NIGEL MAW,CHRISTOPHER PETER WAYMAN
PC          A61K45/00,A61K31/19,A61K31/192,A61K31/4015,A61K31/433,A61K31/
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LOCUS          551 bp      RNA      linear      PAT 27-AUG-2002
DEFINITION    Variant preproenkephalin Y, DNA molecule encoding variant signal
              peptide and utilization of the same.
ACCESSION    BD103561
VERSION      BD103561.1 GI:22649135
KEYWORDS     JP 2001526296-A/5.
SOURCE       unidentified
              unclassified.
              1 (bases 1 to 551)
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
Original source text: Human pheochromocytoma, cDNA to mRNA, clone
pNPY3-75.
Neuropeptide Y (NPY) is one of the most abundant peptides in the
mammalian nervous system, and its extensive distribution suggests a
neuro-transmitter or -modulator role. NPY is also found in some
chromaffin cells of the adrenal medulla.
              Location/Qualifiers

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Koulu,M., Karvonen,M., Pesonen,U. and Uusitupa,M.
Variant preproenkephalin Y, DNA molecule encoding variant signal
peptide and utilization of the same
Patent: JP 2001526296-A 5 18-DEC-2001;
HORMOS MEDICAL OY LTD
OS          Unidentified
PN          JP 2001526296-A/5
PD          18-DEC-2001
PR          16-DEC-1998 JP 2000525455
PR          19-DEC-1997 US 08/994946
PI          MARKKU KOULU,MATTI KARVONEN,ULLAMARI PESONEN,MATTI UUSITUPA PC
A61P43/00,
C07K14/575,A01K67/027,A61K38/00,A61K38/22,A61K48/00,A61P3/06, PC
PC          C07K16/26,C12N5/10,C12N15/09,C12Q1/68,G01N33/15,G01N33/50// PC
C12P21/08,
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CC          Topology: Linear;
CC          Variant preproenkephalin Y, DNA molecule encoding variant
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CC          and utilization of the same
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RESULT 10
HUMNPY
LOCUS          551 bp      mRNA      linear      PRI 07-JAN-1995
DEFINITION    Human neuropeptide Y (NPY) mRNA, complete cds.
ACCESSION    K01911
VERSION      K01911.1 GI:189273
KEYWORDS     neuropeptide Y.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 551)
REFERENCE    Minth,C.D., Bloom,S.R., Polak,J.M. and Dixon,J.E.
AUTHORS     Cloning, characterization, and DNA sequence of a human cDNA
              encoding neuropeptide tyrosine
TITLE       Proc. Natl. Acad. Sci. U.S.A. 81 (14), 4577-4581 (1984)
JOURNAL      84272678
MEDLINE
PUBMED      6589611
COMMENT
Original source text: Human pheochromocytoma, cDNA to mRNA, clone
pNPY3-75.
Neuropeptide Y (NPY) is one of the most abundant peptides in the
mammalian nervous system, and its extensive distribution suggests a
neuro-transmitter or -modulator role. NPY is also found in some
chromaffin cells of the adrenal medulla.
              Location/Qualifiers

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source
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/db_xref="taxon:9606"
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/tissue_type="pheochromocytoma"
gene
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<1. .551
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/mnote="G00-119-456"
CDS
87. .380
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/protein_id="AAA59944.1"
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87. .170
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/mnote="G00-119-456"
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171. .278
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/note="G00-119-456"
ORIGIN
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Query Match 100.0%; Score 138; DB 9; Length 551;
Best Local Similarity 100.0%; Pred. No. 4.6e-23;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60
Db 1 ACCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60

QY 61 CCAGCCACGCCCGCGCCGACCAACCATGCTAGGTAAACAAGCGACTGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGCCGACCAACCATGCTAGGTAAACAAGCGACTGGGCTGTCCGGAC 120

QY 121 TGACCCCTGCCTGTCCC 138
Db 121 TGACCCCTGCCTGTCCC 138

RESULT 11
G18330
LOCUS
DEFINITION
G18330 SW51475 Eric D. Green Homo sapiens STS genomic, sequence tagged
site.
ACCESSION
G18330
VERSION
G18330.1 GI:1222787
KEYWORDS
STS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 551)
Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,
Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,
Leckie,M.P. and Green,E.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
97189344
MEDLINE
PUBMED
9037602
REFERENCE
2 (bases 1 to 551)
Green,E.D.
Homo sapiens
Human chromosome 7 STSs (1997)
AUTHORS
Unpublished (1997)
JOURNAL
Synonyms: NPY
COMMENT
GDB: GDB:3754247
GDB_DSEG: NPY

```

Contact: Eric D. Green  
Genome Technology Branch  
National Human Genome Research Institute/NIH  
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892  
Tel: 3014020201  
Fax: 3014024735  
Email: egreen@nhgri.nih.gov  
Primer A: CCACCCATCCTTACCAATG  
Primer B: GACAAAGGAACACATTGCAG  
STS size: 60  
PCR Profile:

Presoak: 0 degrees C for 0.00 minute(s)  
Denaturation: 92 degrees C for 0.17 minute(s)  
Annealing: 55 degrees C for 1.00 minute(s)  
Polymerization: 72 degrees C for 1.00 minute(s)  
PCR Cycles: 35  
Thermal Cycler: PerkinElmer 9600

Protocol:  
Template: 30-100 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/ul  
Total Vol: 10 ul

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 8.3

This STS was developed from sequence determined by another investigator. See GenBank record: K01911 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/STB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID=92128937].

#### FEATURES

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/db\_xref="taxon:9606"  
/map="7"  
clone\_lib="Eric D. Green"  
1. .551  
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primer\_bind  
primer\_bind  
complement(490. .509)

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Query Match 100.0%; Score 138; DB 11; Length 551;  
Best Local Similarity 100.0%; Pred. No. 4.6e-23;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60  
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Qy 61 CCAGCCACGCCCGCGCCGACCAACCATGCTAGGTAAACAAGCGACTGGGCTGTCCGGAC 120  
Db 61 CCAGCCACGCCCGCGCGCCGACCAACCATGCTAGGTAAACAAGCGACTGGGCTGTCCGGAC 120  
Qy 121 TGACCCCTGCCTGTCCC 138  
Db 121 TGACCCCTGCCTGTCCC 138

RESULT 12  
BC029497  
LOCUS  
DEFINITION  
Homo sapiens neuropeptide Y, mRNA (cdna clone MGC:33138  
IMAGE:5278692), complete cds.

BC029497 568 bp mRNA linear PRI 06-OCT-2003  
Homo sapiens neuropeptide Y, mRNA (cdna clone MGC:33138  
IMAGE:5278692), complete cds.

[illegible]

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 122)  
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.  
TITLE EST and encoded human protein  
JOURNAL Patent: JP 2002010789-A 4367 15-JAN-2002;  
GENSET CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002010789-A/4367  
PD 15-JAN-2002  
PF 07-AUG-2000 JP 2000280989  
PR 05-AUG-1999 US 60/147499  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI  
GIORDANO  
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC  
C12N1/21,  
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC  
C12N15/00  
CC EST and encoded human protein  
FH Key Location/Qualifiers  
FT source 1..122  
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FT /organism='Homo sapiens (human)'.  
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/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
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Query Match 82.0%; Score 113.2; DB 6; Length 122;  
Best Local Similarity 94.3%; Pred. No. 4.8e-17;  
Matches 115; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 ACCCCATCGCTGGCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
DB 1 ACCCCATCGCTGGCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTG 107  
DB 270 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTGCTACGACCCGCTCTG 316  
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Job time : 862 secs  
RESULT 15  
AR176715 325 bp DNA linear PAT 17-DEC-2001  
LOCUS  
DEFINITION Sequence 1 from patent US 6312898.  
ACCESSION AR176715  
VERSION AR176715.1 GI:17919070  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 325)  
AUTHORS Koulou,M., Karvonen,M., Pesonen,U. and Uusitupa,M.  
TITLE Diagnosis of a person's risk of developing atherosclerosis or  
diabetic retinopathy based on leucine 7 to proline 7 polymorphism  
in the prepro-neuropeptide Y gene  
JOURNAL Patent: US 6312898-A 1 06-NOV-2001;  
FEATURES  
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Best Local Similarity 90.7%; Pred. No. 8.1e-12;  
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCCATCGCTGGCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
DB 210 ACCCCATCGCTGGCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 269  
QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTG 107  
DB 270 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTGCTACGACCCGCTCTG 316

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 272 Seconds  
(without alignments)

2155.336 Million cell updates/sec

Title: US-09-645-590-1

Perfect score: 138

Sequence: 1 accccatcgctgctctca.....actgacctcgccgtgcc 138

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_29Jan04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002s.\*

7: Geneseqn2003as.\*

8: Geneseqn2003bs.\*

9: Geneseqn2003cs.\*

10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	138	100.0	138	6 AAL42206	Aal42206 Human neu
2	138	100.0	138	6 AAL42205	Aal42205 Human neu
3	138	100.0	551	2 AAX86051	Aax86051 cDNA enco
4	138	100.0	551	3 AAC60348	Aac60348 Human neu
5	138	100.0	551	4 AAD14527	Aad14527 Human neu
6	138	100.0	551	4 AAD14517	Aad14517 Human neu
7	138	100.0	551	4 AAF84086	Aaf84086 Human neu
8	138	100.0	551	6 AAF84076	Aaf84076 Human neu
9	138	100.0	551	6 ABL69726	Ab169726 Prostate
10	138	100.0	551	6 ABN84276	Abn84276 Human neu
11	138	100.0	551	6 AAL47339	Aal47339 Human neu
12	138	100.0	551	7 ACF63372	Acf63372 Human neu
13	124.8	90.4	969	4 AAF72746	Aaf72746 Human pro
14	111	80.4	553	4 AAF72771	Aaf72771 Human pro
15	111	80.4	599	3 AAF15665	Aaf15665 Human pro
16	111	80.4	599	4 AAF72772	Aaf72772 Human pro
17	91	65.9	325	2 AAX86047	Aax86047 Exon 1 of
18	91	65.9	325	3 AAC60344	Aac60344 Human neu
19	91	65.9	325	6 AAL47340	Aal47340 Human neu
20	91	65.9	722	6 AAL47344	Aal47344 Human neu
21	91	65.9	14537	6 AAL48078	Aal48078 Human neu
22	90.8	65.8	609	5 ABV35249	Abv35249 Human pro
23	90.8	65.8	609	5 ABV44088	Abv44088 Human pro

24	89.4	64.8	496	8	ACH15527	Human adu
25	89.2	64.6	696	5	ABV04986	Human pro
26	89	64.5	683	5	ABV14155	Human pro
27	87	63.0	562	5	ABV23158	Human pro
28	87	63.0	562	3	ABV28999	Human pro
29	84.2	61.0	169	3	AAC09551	Human sec
30	63.2	45.8	539	9	ADB52549	Primary r
31	63.2	45.8	707	6	ABT09021	Phase-1 R
32	63	45.7	483	6	ABT09021	Mouse isc
33	63	45.7	1185	5	ABV29161	Human pro
34	63	45.7	1185	5	ABV21898	Human pro
35	63	45.7	1185	5	ABV27730	Human pro
36	63	45.7	1185	5	ABV24480	Human pro
37	63	45.7	1185	5	ABV22222	Human pro
38	63	45.7	1185	5	ABV22776	Human pro
39	63	45.7	1185	5	ABV21541	Human pro
40	63	45.7	1185	5	ABV27360	Human pro
41	63	45.7	1185	5	ABV28602	Human pro
42	63	45.7	1185	5	ABV23315	Human pro
43	63	45.7	1185	5	ABV28059	Human pro
44	62.8	45.5	417	9	ADB75464	Prostate
45	52	37.7	247	2	AX86048	Exon 2 of

#### ALIGNMENTS

RESULT 1  
AAL42206  
ID AAL42206 standard; mRNA; 138 BP.  
XX  
AC AAL42206;  
XX  
DT 13-JUN-2002 (first entry)  
XX  
DE Human neurotensin Y (NPY) mRNA sequence, binding structure 2.  
XX  
KW Human; ss; stress-induced neurotensin Y overproduction; NPY;  
KW neurotransmitter; central nervous system; peripheral nervous system;  
KW heart rate reduction; insulin secretion enhancement; NPY mRNA;  
KW binding structure 2.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT stem\_loop 10..38 /\*tag= a  
FT misc\_binding 41..46 /\*tag= b  
FT /\*bound moiety= "Human neurotensin Y (NPY) mRNA"  
FT /\*note= "Forms a double stranded region with bases 115-110 of itself"  
FT stem\_loop 50..68 /\*tag= c  
FT stem\_loop 70..109 /\*tag= d  
FT misc\_binding 110..115 /\*tag= e  
FT /\*bound moiety= "Human neurotensin Y (NPY) mRNA"  
FT /\*note= "Forms a double stranded region with bases 46-41 of itself"  
FT stem\_loop 117..137 /\*tag= f  
WO200215941-A1.  
28-FEB-2002.  
31-JUL-2001; 2001WO-FI000687.  
25-AUG-2000; 2000US-00645590.  
(HORM-) HORMOS MEDICAL CORP.

XX Koulou M, Karvonen M, Pesonen U, Uusitupa M, Kallio J;  
 PI WPI; 2002-269319/31.  
 XX  
 DR  
 XX  
 PT Reducing stress-induced overproduction of neuropeptide Y (NPY) in an  
 PT individual useful for reducing heart rate and enhancing insulin  
 XX secretion.  
 PS Disclosure; Page 23; 45pp; English.  
 XX  
 CC The invention comprises a method for reducing stress-induced  
 CC overproduction of neuropeptide Y (NPY) in an individual. NPY is the most  
 CC abundant neuropeptide and an important neurotransmitter in the human  
 CC central and peripheral nervous system. The method of the invention is  
 CC useful for reducing constitutive overexpression of NPY in the endothelial  
 CC cells of an individual, in order to reduce the heart rate and enhance  
 CC insulin secretion. The method of the invention is also useful for  
 CC diagnosing susceptibility to stress-induced overproduction of NPY. The  
 CC present sequence represents binding structure 2 of the human NPY mRNA  
 XX  
 SQ Sequence 138 BP; 23 A; 61 C; 34 G; 20 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 138; DB 6; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-30;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCGTCCGCCGACAGCATAGTACTTGGCCG 60  
 Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCGTCCGCCGACAGCATAGTACTTGGCCG 60  
 QY 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120  
 Db 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCTCGCCCTGTCCC 138  
 Db 121 TGACCTCGCCCTGTCCC 138  
 RESULT 2  
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 ID AAL42205 standard; mRNA; 138 BP.  
 AC AAL42205;  
 XX  
 DT 13-JUN-2002 (first entry)  
 XX  
 DE Human neuropeptide Y (NPY) mRNA sequence, binding structure 1.  
 XX  
 KW Human; ss; stress-induced neuropeptide Y overproduction; NPY;  
 KW neurotransmitter; central nervous system; peripheral nervous system;  
 KW heart rate reduction; insulin secretion enhancement; NPY mRNA;  
 KW binding structure 1.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT stem\_loop 10..38  
 FT /\*tag= a  
 FT stem\_loop 41..115  
 FT /\*tag= b  
 FT stem\_loop 117..137  
 FT /\*tag= c  
 FT  
 PN WO2002I5941-A1.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 31-JUL-2001; 2001WO-FI000687.  
 XX  
 PR 25-AUG-2000; 2000US-00645590.  
 XX

PA (HORM-) HORMOS MEDICAL CORP.  
 XX Koulou M, Karvonen M, Pesonen U, Uusitupa M, Kallio J;  
 PI WPI; 2002-269319/31.  
 XX  
 DR  
 XX  
 PT Reducing stress-induced overproduction of neuropeptide Y (NPY) in an  
 PT individual useful for reducing heart rate and enhancing insulin  
 XX secretion.  
 PS Disclosure; Page 22; 45pp; English.  
 XX  
 CC The invention comprises a method for reducing stress-induced  
 CC overproduction of neuropeptide Y (NPY) in an individual. NPY is the most  
 CC abundant neuropeptide and an important neurotransmitter in the human  
 CC central and peripheral nervous system. The method of the invention is  
 CC useful for reducing constitutive overexpression of NPY in the endothelial  
 CC cells of an individual, in order to reduce the heart rate and enhance  
 CC insulin secretion. The method of the invention is also useful for  
 CC diagnosing susceptibility to stress-induced overproduction of NPY. The  
 CC present sequence represents binding structure 1 of the human NPY mRNA  
 XX  
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 Query Match 100.0%; Score 138; DB 6; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-30;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCGTCCGCCGACAGCATAGTACTTGGCCG 60  
 QY 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120  
 Db 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCTCGCCCTGTCCC 138  
 Db 121 TGACCTCGCCCTGTCCC 138  
 RESULT 3  
 AAX86051  
 ID AAX86051 standard; cDNA; 551 BP.  
 AC AAX86051;  
 XX  
 DT 14-SEP-1999 (first entry)  
 XX  
 DE cDNA encoding human prepro-neuropeptide Y (NPY).  
 XX  
 KW Human neuropeptide Y; NPY; prepro-neuropeptide Y; mutant;  
 KW serum cholesterol; low density lipoprotein; LDL; db.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 87..380  
 FT /\*tag= a  
 FT sig\_peptide 87..170  
 FT /\*tag= b  
 FT mutation 106  
 FT /\*tag= c  
 FT /note= "this base is changed to C to encode the mutant  
 FT protein of the invention"  
 FT  
 PN WO9932518-A1.  
 XX  
 PD 01-JUL-1999.  
 XX  
 PF 16-DEC-1998; 98WO-FI000985.  
 XX  
 PR 19-DEC-1997; 97US-00994946.

XX PA (HORM-) HORMOS MEDICAL LTD OY.  
 XX PI Koulu M, Karvonen M, Pesonen U, Uusitupa M;  
 XX WPI; 1999-405161/34.  
 DR P-PSDB; AAY2382B.  
 XX  
 XX New polynucleotide (I) encoding a prepro-neuropeptide Y (preproNPY).  
 XX Claim 2; Fig 1c; 45pp; English.  
 XX  
 CC The present sequence encodes human prepro-neuropeptide Y (NPY). The  
 CC specification describes a polynucleotide encoding a prepro-neuropeptide Y  
 CC (preproNPY), where leu (7) is substituted by pro(7). This polynucleotide  
 CC is useful for diagnosing and treating humans with a predisposition for  
 CC increased serum cholesterol or low density lipoprotein (LDL)  
 XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
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 Query Match 100.0%; Score 138; DB 2; Length 551;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60  
 QY 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120  
 Db 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120  
 QY 121 TGACCCCTCGCCCTGTCCC 138  
 Db 121 TGACCCCTCGCCCTGTCCC 138  
 RESULT 4  
 AAC60348  
 ID AAC60348 standard; DNA; 551 BP.  
 AC AAC60348;  
 XX  
 XX 16-FEB-2001 (first entry)  
 XX Human neuropeptide Y coding DNA.  
 XX NPY; neuropeptide Y; gene therapy; atherosclerosis; diabetic retinopathy;  
 KW ds.  
 KW Homo sapiens.  
 XX  
 XX WO200063430-A1.  
 XX 26-OCT-2000.  
 XX 29-MAR-2000; 2000WO-FI000260.  
 XX 15-APR-1999; 99US-00291994.  
 XX (HORM-) HORMOS MEDICAL LTD OY.  
 XX Koulu M, Karvonen M, Pesonen U, Uusitupa M;  
 XX WPI; 2000-679606/66.  
 XX  
 XX Diagnosing diabetic person's susceptibility for developing  
 XX atherosclerosis or diabetic retinopathy involves detecting leucine7 to  
 XX proline7 polymorphism in signal peptide part of human prepro neuropeptide  
 XX Y.  
 XX Disclosure; Fig 1; 4lpp; English.

CC The present invention relates to diagnosing a diabetic person's  
 CC susceptibility for having an increased risk of developing atherosclerosis  
 CC or diabetic retinopathy involves determining whether the subject has a  
 CC substitution of leucine 7 for proline in the signal peptide part of human  
 XX preproneuropeptide Y  
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 138; DB 3; Length 551;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60  
 QY 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120  
 Db 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120  
 QY 121 TGACCCCTCGCCCTGTCCC 138  
 Db 121 TGACCCCTCGCCCTGTCCC 138  
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 ID AAD14527 standard; DNA; 551 BP.  
 XX  
 XX AAD14527;  
 XX  
 XX 01-NOV-2001 (first entry)  
 XX Human neuropeptide Y (NPY) DNA.  
 XX Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;  
 KW FSAD; neutral endopeptidase inhibitor; I:NEP; enkephalinase;  
 KW gynaecological; endopeptidase-2; neuropeptide Y; NPY; ds.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 87..380  
 FT /\*tag= a  
 FT /product= "Human NPY"  
 FT sig\_peptide 87..170  
 FT /\*tag= b  
 FT mat\_peptide 171..278  
 FT /\*tag= c  
 FT /product= "Human mature NPY protein"  
 XX  
 XX EPI097719-A1.  
 XX  
 XX 09-MAY-2001.  
 XX  
 XX 03-NOV-2000; 2000EP-00309722.  
 XX  
 XX 08-NOV-1999; 99GB-00026437.  
 XX 18-FEB-2000; 2000GB-00004021.  
 XX 26-MAY-2000; 2000GB-00013001.  
 XX 05-JUL-2000; 2000GB-00016563.  
 XX 12-JUL-2000; 2000GB-00017141.  
 XX (PFIZ ) PFIZER LTD.  
 XX (PFIZ ) PFIZER INC.  
 XX  
 XX Maw GN, Wayman CP;  
 XX WPI; 2001-309880/33.  
 XX P-PSDB; AAE07955.  
 XX  
 XX Treating females suffering from female sexual dysfunction, preferably  
 XX female sexual arousal dysfunction using a neutral endopeptidase inhibitor

PT that potentiates cAMP in female genitalia.  
 PS Disclosure; Page 97; 124pp; English.  
 XX  
 CC The present invention relates to a method for treating female sexual  
 CC dysfunction (FSD), preferably female sexual arousal dysfunction (FSAD).  
 CC The method comprising using an agent, an inhibitor of neutral  
 CC endopeptidase (NEP) EC 3.4.24.11 or I-NEP, which is capable of  
 CC potentiating cAMP (which enhances female genital blood flow) in the  
 CC sexual genitalia of the females. NEP is also known as enkephalinase or  
 CC endopeptidase-2. The agent is optionally admixed with a diluent, carrier  
 CC or excipient. The method restores a normal sexual arousal response,  
 CC particularly increased blood flow leading to vaginal, clitoral and labial  
 CC engorgement. This will result in increased vaginal lubrication via plasma  
 CC transduction, increased vaginal compliance and increased genital (e.g.  
 CC vaginal and clitoral) sensitivity. The present sequence is human  
 CC neuropeptide Y (NPY) DNA used in the method of the invention  
 XX  
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 138; DB 4; Length 551;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60  
 DB 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60  
 QY 61 CCAGCCAGCCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120  
 DB 61 CCAGCCAGCCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCCCTCGCCCTGTGCC 138  
 DB 121 TGACCCCTCGCCCTGTGCC 138  
 RESULT 6  
 AAD14517  
 ID AAD14517 standard; DNA; 551 BP.  
 XX  
 AC AAD14517;  
 DT 01-NOV-2001 (first entry)  
 DE Human neuropeptide Y (NPY) DNA.  
 KW Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;  
 KW FSAD; neuropeptide Y; NPY; gynaecological; vasoactive intestinal peptide;  
 KW VIP; ds.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 87..380  
 FT /\*tag= a  
 FT sig\_peptide /product= "Human NPY protein"  
 FT 87..170  
 FT /\*tag= b  
 FT mat\_peptide 171..278  
 FT /\*tag= c  
 FT /product= "Human mature NPY protein"  
 XX  
 EP1097718-Al.  
 XX  
 PD 09-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000EP-00309720.  
 XX  
 PR 08-NOV-1999; 99GB-00026437.  
 PR 18-FEB-2000; 2000GB-00004021.  
 PR 26-MAY-2000; 2000GB-00013001.  
 PR 05-JUL-2000; 2000GB-00016563.

PR 12-JUL-2000; 2000GB-00017141.  
 XX  
 PA (PFIZ ) PFIZER LTD.  
 PA (PFIZ ) PFIZER INC.  
 XX  
 PI Maw GN, Wayman CP;  
 DR WPI; 2001-319199/34.  
 DR P-PSDB; AAE07919.  
 XX  
 PT Treating females suffering from female sexual dysfunction, preferably  
 PT female sexual arousal dysfunction using a neuropeptide Y inhibitor that  
 PT potentiates cAMP in female genitalia.  
 XX  
 PS Disclosure; Page 129; 165pp; English.  
 XX  
 CC The patent discloses a method for the treatment of a female suffering  
 CC from female sexual dysfunction (FSD), preferably female sexual arousal  
 CC dysfunction (FSAD) by the use of an agent which is an inhibitor of  
 CC neuropeptide Y (NPY). The agent is capable of potentiating cAMP which  
 CC enhances female genital (e.g. vaginal or clitoral) blood flow in the  
 CC sexual genitalia of the female and is optionally admixed with a diluent  
 CC carrier or excipient. The method restores a normal sexual arousal  
 CC response namely, increased blood flow leading to vaginal, clitoral and  
 CC labial engorgement. This will result in increased vaginal lubrication via  
 CC plasma transduction, increased vaginal compliance and increased genital  
 CC (e.g. vaginal and clitoral) sensitivity. The method is used for treating  
 CC a female suffering from FSD preferably FSAD. The present sequence is a  
 CC DNA encoding human neuropeptide Y (NPY) protein. NPY exerts an inhibitory  
 CC influence over VIP-mediated vasorelaxation and NPY Y1 receptor  
 CC antagonists will facilitate the vasoactive effect of endogenous  
 CC vasoactive intestinal peptide (VIP) released during arousal and enhances  
 CC vaginal engorgement  
 XX  
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 138; DB 4; Length 551;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;  
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60  
 DB 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60  
 QY 61 CCAGCCAGCCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120  
 DB 61 CCAGCCAGCCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCCCTCGCCCTGTGCC 138  
 DB 121 TGACCCCTCGCCCTGTGCC 138  
 RESULT 7  
 AAF84086  
 ID AAF84086 standard; DNA; 551 BP.  
 XX  
 AC AAF84086;  
 DT 22-AUG-2001 (first entry)  
 DE Human neuropeptide Y (NPY) encoding DNA.  
 KW Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;  
 KW genital; vaginal; clitoral; blood flow; cAMP; phosphodiesterase; PDE;  
 KW cGMP; medicament; human; neuropeptide Y; NPY; ds.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 87..380  
 FT /\*tag= a  
 FT /product= "neuropeptide Y"



```
FT sig_peptide /gene= "NPY"
FT 87..170
FT /*tag= b
FT 171..377
FT mat_peptide /*tag= c
FT
PN EPI097706-A1.
XX
XX 09-MAY-2001.
XX
XX 03-NOV-2000; 2000EP-00309719.
XX
XX 08-NOV-1999; 99GB-00026437.
XX 18-FEB-2000; 2000GB-00004021.
XX 26-MAY-2000; 2000GB-00013001.
XX 05-JUL-2000; 2000GB-00016563.
XX 12-JUL-2000; 2000GB-00017141.
XX
XX (PFIZ ) PFIZER LTD.
XX (PFIZ ) PFIZER INC.
XX
XX Maw GN, Wayman CP;
XX
XX WPI; 2001-383217/41.
XX P-PSDB; AAB85118.
XX
XX Novel pharmaceutical composition for treating female sexual dysfunction,
XX preferably female sexual arousal disorder, comprising an agent capable of
XX potentiating cAMP in the sexual genitalia of the female.
XX
XX Disclosure; Page 104; 135pp; English.
XX
XX The invention provides a pharmaceutical composition for treating female
XX sexual dysfunction (FSD), preferably female sexual arousal disorder
XX (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow
XX in a female. The composition comprises an agent capable of potentiating
XX cAMP in the sexual genitalia of the female. The agent is an inhibitor
XX (1:PDE) of phosphodiesterase (PDE), which hydrolyzes cAMP (optionally
XX cGMP). The agent is useful in the manufacture of a medicament for the
XX treatment of FSD, preferably FSAD, by potentiating cAMP in the sexual
XX genitalia. It is also useful in the manufacture of a medicament for
XX enhancing female genital (e.g., vaginal or clitoral) blood flow. The
XX present sequence represents a human neuropeptide Y (NPY) encoding DNA
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 138; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
DB 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
QY 61 CCAGCCACGCGCCGCGCCAGCCACCATGCTAGTACACAGCGACTGGGCTGTCCGGAC 120
DB 61 CCAGCCACGCGCCGCGCCAGCCACCATGCTAGTACACAGCGACTGGGCTGTCCGGAC 120
QY 121 TGACCCCTGCGCCCTGTCCC 138
DB 121 TGACCCCTGCGCCCTGTCCC 138
RESULT 8
ID AAF84076
XX AAF84076 standard; DNA; 551 BP.
XX
XX AAF84076;
XX
XX 22-AUG-2001 (first entry)
XX
XX Human neuropeptide Y (NPY) encoding DNA.
XX
```

```
KW Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
KW genital; vaginal; clitoral; blood flow; cAMP; phosphodiesterase; PDE;
XX cGMP; medicament; human; neuropeptide Y; NPY; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 87..380
XX /*tag= a
XX /product= "neuropeptide Y"
XX /gene= "NPY"
XX sig_peptide 87..170
XX /*tag= b
XX mat_peptide 171..377
XX /*tag= c
XX
XX EPI097706-A1.
XX
XX 09-MAY-2001.
XX
XX 03-NOV-2000; 2000EP-00309718.
XX
XX 08-NOV-1999; 99GB-00026437.
XX 18-FEB-2000; 2000GB-00004021.
XX 26-MAY-2000; 2000GB-00013001.
XX 05-JUL-2000; 2000GB-00016563.
XX 12-JUL-2000; 2000GB-00017141.
XX
XX (PFIZ ) PFIZER LTD.
XX (PFIZ ) PFIZER INC.
XX
XX Maw GN, Wayman CP;
XX
XX WPI; 2001-383216/41.
XX P-PSDB; AAB85107.
XX
XX Novel pharmaceutical composition for treating female sexual dysfunction,
XX preferably female sexual arousal disorder, comprising an agent capable of
XX potentiating cAMP in the sexual genitalia of the female.
XX
XX Disclosure; Page 102; 132pp; English.
XX
XX The invention provides a pharmaceutical composition for treating female
XX sexual dysfunction (FSD), preferably female sexual arousal disorder
XX (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow
XX in a female. The composition comprises an agent capable of potentiating
XX cAMP in the sexual genitalia of the female. The agent is an inhibitor
XX (1:PDE) of phosphodiesterase (PDE), which hydrolyzes cAMP (optionally
XX cGMP). The agent is useful in the manufacture of a medicament for the
XX treatment of FSD, preferably FSAD, by potentiating cAMP in the sexual
XX genitalia. It is also useful in the manufacture of a medicament for
XX enhancing female genital (e.g., vaginal or clitoral) blood flow. The
XX present sequence represents a human neuropeptide Y (NPY) encoding DNA
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 138; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
DB 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
QY 61 CCAGCCACGCGCCGCGCCAGCCACCATGCTAGTACACAGCGACTGGGCTGTCCGGAC 120
DB 61 CCAGCCACGCGCCGCGCCAGCCACCATGCTAGTACACAGCGACTGGGCTGTCCGGAC 120
QY 121 TGACCCCTGCGCCCTGTCCC 138
DB 121 TGACCCCTGCGCCCTGTCCC 138
```

RESULT 9  
ABL69726  
ID ABL69726 standard; DNA; 551 BP.  
XX AC ABL69726;  
XX  
DT 15-MAY-2002 (first entry)  
XX  
DE Prostate cancer related gene sequence SEQ ID NO:8063.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US010838.  
XX  
PR 05-JUN-2000; 2000US-0209473P.  
PR 05-JUN-2000; 2000US-0209531P.  
PR 18-SEP-2000; 2000US-0233133P.  
PR 18-SEP-2000; 2000US-0233617P.  
PR 20-SEP-2000; 2000US-0234009P.  
PR 20-SEP-2000; 2000US-0234034P.  
PR 20-SEP-2000; 2000US-0234052P.  
PR 22-SEP-2000; 2000US-0234509P.  
PR 22-SEP-2000; 2000US-0234567P.  
PR 25-SEP-2000; 2000US-0234923P.  
PR 25-SEP-2000; 2000US-0234924P.  
PR 25-SEP-2000; 2000US-0235077P.  
PR 25-SEP-2000; 2000US-0235082P.  
PR 25-SEP-2000; 2000US-0235134P.  
PR 25-SEP-2000; 2000US-0235280P.  
PR 26-SEP-2000; 2000US-0235637P.  
PR 26-SEP-2000; 2000US-0235638P.  
PR 27-SEP-2000; 2000US-0235711P.  
PR 27-SEP-2000; 2000US-0235720P.  
PR 27-SEP-2000; 2000US-0235840P.  
PR 27-SEP-2000; 2000US-0235863P.  
PR 28-SEP-2000; 2000US-0236028P.  
PR 28-SEP-2000; 2000US-0236032P.  
PR 28-SEP-2000; 2000US-0236033P.  
PR 28-SEP-2000; 2000US-0236034P.  
PR 28-SEP-2000; 2000US-0236109P.  
PR 28-SEP-2000; 2000US-0236111P.  
PR 29-SEP-2000; 2000US-0236842P.  
PR 29-SEP-2000; 2000US-0236891P.  
PR 02-OCT-2000; 2000US-0237172P.  
PR 02-OCT-2000; 2000US-0237173P.  
PR 02-OCT-2000; 2000US-0237278P.  
PR 02-OCT-2000; 2000US-0237294P.  
PR 02-OCT-2000; 2000US-0237295P.  
PR 02-OCT-2000; 2000US-0237316P.  
PR 03-OCT-2000; 2000US-0237425P.  
PR 03-OCT-2000; 2000US-0237598P.  
PR 03-OCT-2000; 2000US-0237604P.  
PR 03-OCT-2000; 2000US-0237606P.  
PR 03-OCT-2000; 2000US-0237608P.  
PR 01-NOV-2000; 2000US-0244867P.  
PR 01-NOV-2000; 2000US-0245084P.  
XX  
XX (AVAL-) AVALON PHARM.  
XX  
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
XX WPI; 2002-198264/24.  
XX

PT Screening for anti-neoplastic agent involves exposing cells to a chemical  
PT agent to be tested for anti-neoplastic activity, and determining a change  
XX in expression of a gene of a signature gene set.  
PS Claim 1; SEQ ID NO 8063; 44pp; English.  
XX  
CC The present invention describes a method (M1) for screening for an anti-  
CC neoplastic agent. The method involves exposing cells to a chemical agent  
CC to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
CC to ABL70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening an  
CC anti-neoplastic agent, and can be used for producing a product which is  
CC the data collected with respect to the anti-neoplastic agent as a result  
CC of M1, and the data is sufficient to convey the chemical structure and/or  
CC properties of the agent. M1 can be used in the treatment of cancer such  
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's  
CC tumour  
XX  
SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 138; DB 6; Length 551;  
Best Local Similarity 100.0%; Pred. No. 2.6e-30;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGATAGTACTTGCCTG 60  
DB 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGATAGTACTTGCCTG 60  
QY 61 CCAGCCAGCCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGGACTGGGGCTGTCCGGAC 120  
DB 61 CCAGCCAGCCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGGACTGGGGCTGTCCGGAC 120  
QY 121 TGACCTCGCCCTGTCTCC 138  
DB 121 TGACCTCGCCCTGTCTCC 138  
RESULT 10  
ABN84276  
ID ABN84276 standard; cDNA; 551 BP.  
XX AC ABN84276;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human neuropeptide Y nucleotide sequence.  
XX  
KW Neuropeptide Y; NPY; human; inhibitor; male sexual dysfunction;  
KW male erectile dysfunction; obesity; anorexia; bulimia; vasotropic;  
KW anorectic; therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200247670-A1.  
XX  
PD 20-JUN-2002.  
XX  
PF 10-DEC-2001; 2001WO-IB002399.  
XX  
PR 15-DEC-2000; 2000GB-00030647.  
PR 06-APR-2001; 2001GB-00008730.  
PR 23-APR-2001; 2001GB-00009910.  
PR 04-MAY-2001; 2001GB-00011037.  
PR 29-JUN-2001; 2001US-00895367.  
PR 13-JUL-2001; 2001US-00905846.  
PR 24-AUG-2001; 2001US-00020679.  
XX

```
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
XX Naylor AM, Van Der Graaf PH, Wayman CP;
XX WPI; 2002-547828/58.
XX
XX Use of an inhibitor of neuropeptide Y in the preparation of medicament
XX for the treatment or prevention of male erectile dysfunction.
XX
XX Disclosure; Fig 4; 179pp; English.
XX
XX The present sequence is a human neuropeptide Y (NPY) polynucleotide
XX sequence. The invention relates to the use of an inhibitor of NPY, or an
XX inhibitor of an NPY Y1 receptor, especially an inhibitor selective for an
XX NPY or NPY Y1 receptor associated with male genitalia, in the preparation
XX of a medicament for the treatment or prevention of male sexual
XX dysfunction, especially male erectile dysfunction (MED). A polypeptide
XX encoded by the present sequence may be used as a target in screens to
XX identify agents capable of inhibiting NPY. NPY may also be used as a
XX target to identify agents capable of mediating an increase in
XX intracavernosal pressure through the inhibition of NPY. The inhibitor
XX selectively increases intracavernosal pressure of the penis which
XX facilitates and/or causes penile erection during sexual arousal. In
XX addition to treatment of MED, the inhibitor can also be used to treat
XX abnormal drink and food intake disorders, such as obesity, bulimia,
XX anorexia and metabolic disorders (all claimed)
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 138; DB 6; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60
QY 61 CAGCCACGCGCCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
Db 61 CAGCCACGCGCCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
QY 121 TGACCCCTGGCCCTGTCCC 138
Db 121 TGACCCCTGGCCCTGTCCC 138
RESULT 11
AAL47339
ID AAL47339 standard; cDNA; 551 BP.
XX
XX AAL47339;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human neuropeptide Y coding sequence.
XX
XX Human; neuropeptide Y; NPY; chromosome 7q15.1; SNP; obesity; BMI;
XX body mass index; single nucleotide polymorphism; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 87..380
XX /*tag= a
XX /*product= "NPY"
XX sig_peptide 87..170
XX /*tag= b
XX variation replace(106,C)
XX /*tag= d
XX mat_peptide 171..380
XX /*tag= c
XX
```

```
PN WO200236825-A1.
XX
XX 10-MAY-2002.
XX
XX 02-NOV-2001; 2001WO-SE002431.
XX
XX 03-NOV-2000; 2000SE-00004035.
XX
XX (PHAA ) PHARMACIA AB.
XX
XX Wahlestedt C, Ding B;
XX
XX WPI; 2002-500129/53.
XX
XX P-PSDB; AAO18054.
XX
XX Diagnosing single nucleotide polymorphism(s) in the human neuropeptide Y
XX (NPY) gene, useful for diagnosing a predisposition to e.g. obesity, by
XX determining the nucleic acid sequence at one or more positions of the NPY
XX gene in the human.
XX
XX Example 5; Page 28-29; 37pp; English.
XX
XX The present invention relates to a method of diagnosing a predisposition
XX to obesity in humans by identifying a single nucleotide polymorphism
XX (SNP) at position 1128 (position 106 of this sequence) of the
XX neuropeptide Y gene. The gene is found at chromosome 7q15.1. The present
XX sequence is the NPY coding sequence
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 138; DB 6; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60
QY 61 CAGCCACGCGCCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
Db 61 CAGCCACGCGCCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
QY 121 TGACCCCTGGCCCTGTCCC 138
Db 121 TGACCCCTGGCCCTGTCCC 138
RESULT 12
ACF63372
ID ACF63372 standard; DNA; 551 BP.
XX
XX ACF63372;
XX
XX 09-OCT-2003 (first entry)
XX
XX Human neuropeptide Y gene SEQ ID NO:94.
XX
XX Human; pharmacological; hypotensive; antilipaeamic; vasotropic; laxative;
XX dermatological; antidepressant; tranquilliser; antiinflammatory; eczema;
XX antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;
XX gynaecological; virucide; vulnery; antiarthritic; antipsoriatic; cold;
XX antimicrobial; cytostatic; litholytic; pathological disorder; depression;
XX abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
XX erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
XX ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
XX constipation; headache; seizure; multiple sclerosis; polymyositis;
XX fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
XX chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
XX chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;
XX inflammation; heart burn; infection; colon cancer; malignant melanoma;
XX skin disorder; gene; ds.
XX
XX Homo sapiens.
XX
XX
```

```
XX WO2003006478-A1.
XX
XX 23-JAN-2003.
XX
XX 10-JUL-2002; 2002WO-US021664.
XX
XX 10-JUL-2001; 2001US-0303820P.
XX
XX (Olig-) OLIGOS ETC INC.
XX
XX Dale RMK, Arrow A, Thompson T;
XX
XX WPI; 2003-221709/21.
XX
XX Composition with a modified oligonucleotide useful for treating a patient
XX with a pathological disorder such as abnormal appetite, hypertension,
XX eczema, anxiety, stress, and cancer.
XX
XX Claim 6; Page 97; 173pp; English.
XX
XX The present invention describes a composition (I) suitable for
XX administration in a mammal, which comprises a modified oligonucleotide
XX (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
XX linked by achiral 5'-3' internucleoside phosphate linkages, where the
XX modified oligonucleotide is complementary to a region of a gene
XX associated with a pathological disorder. Also described: (1) a
XX nutritional supplement comprising (II); and (2) a cosmetic composition
XX comprising (II), where the modified oligonucleotide is complementary to a
XX region of a gene associated with a skin disorder. (I) and (II) can have
XX hypotensive, antihypertensive, vasotropic, dermatological, antidepressant,
XX tranquilizer, antiinflammatory, antitumor, laxative, antimigraine,
XX neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
XX vulnerary, antiarthritic, antipsoriatic, antimicrobial, cytostatic and
XX litholytic activities. (I) can be used for treating a patient with a
XX pathological disorder selected from abnormal appetite, hypertension,
XX hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,
XX depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
XX colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
XX migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
XX fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
XX chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
XX chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,
XX inflammation, heart burn, infection, poison ivy, colon cancer, malignant
XX melanoma, and malignant nasal polyps. The nutritional supplement is
XX useful for supplementing the diet of an individual, and the cosmetic
XX composition is useful for improving the appearance of the skin in an
XX individual with a skin disorder. ACP63279 to ACP63410 represent
XX nucleotide sequence given in the exemplification of the present invention
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 138; DB 7; Length 551;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-30;
XX Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACCCATCGGTGGTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60
XX
XX Db 1 ACCCATCGGTGGTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60
XX
XX QY 61 CCAGCCAGCCCGCGCGGCGAGCCACATGCTAGGTAAACAGCGACTGGGGGTGTCGGGAC 120
XX
XX Db 61 CCAGCCAGCCCGCGCGGCGAGCCACATGCTAGGTAAACAGCGACTGGGGGTGTCGGGAC 120
XX
XX QY 121 TGACCTCGCCCTGTCCC 138
XX
XX Db 121 TGACCTCGCCCTGTCCC 138
XX
XX RESULT 13
XX AAF72746
XX ID AAF72746 standard; cDNA; 969 BP.
XX
XX
```

```
AC AAF72746;
XX
XX 24-APR-2001 (first entry)
XX
XX Human prostate cancer antigen coding sequence #6.
XX
XX Immunosuppressive; nootropic; neuroprotective; antiviral; vulnerary;
XX anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
XX immune disorder; cardiovascular disorder; neurological disease;
XX infection; cancer; cytostatic; antiarthritic; antirheumatic;
XX antiasthmatic; anticonvulsant; vasotropic; vulnerary; human;
XX secreted protein; prostate cancer antigen; ss.
XX
XX Homo sapiens.
XX
XX WO200107476-A1.
XX
XX 01-FEB-2001.
XX
XX 20-JUL-2000; 2000WO-US019666.
XX
XX 21-JUL-1999; 99US-0144972P.
XX 13-AUG-1999; 99US-0148681P.
XX 17-AUG-1999; 99US-0149173P.
XX 06-OCT-1999; 99US-0158004P.
XX 05-APR-2000; 2000US-0194689P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX Rosen CA, Birse C;
XX
XX WPI; 2001-138554/14.
XX P-PSDB; AAB80278.
XX
XX New nucleic acid molecule encoding human secreted prostate cancer
XX antigens, useful for the diagnosis and treatment of disorders such as
XX cancer, leukemia and autoimmune disease.
XX
XX Claim 1; Page 359-360; 433pp; English.
XX
XX The present invention relates to human secreted prostate cancer antigen
XX coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
XX The coding sequences and proteins of the present invention are useful for
XX preventing, treating or ameliorating a medical condition; and for the
XX diagnosis and treatment of diseases and disorders. Diseases and disorders
XX that can be diagnosed and treated include (auto)immune diseases (e.g.
XX graft versus host disease and rheumatoid arthritis), inflammatory and
XX allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
XX cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
XX arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
XX disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
XX retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
XX neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
XX and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
XX viruses or parasites. They may also be useful for wound healing,
XX epithelial cell proliferation, supporting cell culture, tissue
XX regeneration, birth control and as a food additive or preservative. The
XX coding sequences can be used to generate fusion proteins by linking the
XX coding sequences to the human immunoglobulin G FC portion coding sequence
XX (AAF72732) for increasing the stability of the fusion protein as compared
XX to the human protein only
XX
XX Sequence 969 BP; 246 A; 275 C; 225 G; 210 T; 0 U; 13 Other;
XX
XX Query Match 90.4%; Score 124.8; DB 4; Length 969;
XX Best Local Similarity 96.9%; Pred. No. 1.7e-26;
XX Matches 126; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 9 CGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGCCAGCCAC 68
XX
XX Db 250 CGAGNNTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGCCAGCCAC 309
XX
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QY 69 GCCCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCCGACTGACCCCTC 128  
|||||  
Db 310 GCCCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCCGACTGACCCCTC 369  
|||||  
QY 129 GCCCTGTCCC 138  
|||||  
Db 370 GCCCTGTCCC 379  
|||||  
RESULT 14  
AAAF72771  
ID AAF72771 standard; cDNA; 553 BP.  
XX  
AC AAF72771;  
XX  
DT 24-APR-2001 (first entry)  
XX  
DE Human prostate cancer antigen coding sequence #31.  
XX  
KW Immunosuppressive; nontropic; neuroprotective; antiviral; vulnary;  
KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;  
KW immune disorder; cardiovascular disorder; neurological disease;  
KW infection; cancer; cytostatic; antiarthritic; antirheumatic;  
KW antiasthmatic; anticonvulsant; vasotropic; vulnary; human;  
KW secreted protein; prostate cancer antigen; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200107476-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 20-JUL-2000; 2000WO-US019666.  
XX  
PR 21-JUL-1999; 99US-0144972P.  
PR 13-AUG-1999; 99US-0148681P.  
PR 17-AUG-1999; 99US-0149173P.  
PR 06-OCT-1999; 99US-0158004P.  
PR 05-APR-2000; 2000US-0194689P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
PI Rosen CA, Birse C;  
XX  
XX WPI; 2001-138554/14.  
DR P-PSDB; AAB80303.  
XX  
PT New nucleic acid molecule encoding human secreted prostate cancer  
PT antigens, useful for the diagnosis and treatment of disorders such as  
PT cancer, leukemia and autoimmune disease.  
XX  
PS Claim 1; Page 375; 433pp; English.  
XX  
CC The present invention relates to human secreted prostate cancer antigen  
CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).  
CC The coding sequences and proteins of the present invention are useful for  
CC preventing, treating or ameliorating a medical condition; and for the  
CC diagnosis and treatment of diseases and disorders. Diseases and disorders  
CC that can be diagnosed and treated include (auto)immune diseases (e.g.  
CC graft versus host disease and rheumatoid arthritis), inflammatory and  
CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.  
CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and  
CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive  
CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.  
CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma), epilepsy  
CC and neurological disorders (e.g. Alzheimer's, Parkinson's disease, Creutzfeldt-Jakob disease) and infections caused by bacteria, fungi,  
CC viruses or parasites. They may also be useful for wound healing,  
CC epithelial cell proliferation, supporting cell culture, tissue  
CC regeneration, birth control and as a food additive or preservative. The  
CC coding sequences can be used to generate fusion proteins by linking the  
CC coding sequences to the human immunoglobulin G FC portion coding sequence

CC (AAF72732) for increasing the stability of the fusion protein as compared  
CC to the human protein only  
XX  
SQ Sequence 553 BP; 148 A; 161 C; 125 G; 119 T; 0 U; 0 Other;  
Query Match 80.4%; Score 111; DB 4; Length 553;  
Best Local Similarity 99.2%; Pred. No. 1.5e-22;  
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 16 TCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCCGCGG 75  
|||||  
Db 1 TCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCCGCGG 60  
|||||  
QY 76 CGCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGACTGACCTCGCCCTGT 135  
|||||  
Db 61 CGCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGACTGA-CCTGGCCCTGT 119  
|||||  
QY 136 CCC 138  
|||||  
Db 120 CCC 122  
|||||  
RESULT 15  
AAAF15665  
ID AAF15665 standard; cDNA; 599 BP.  
XX  
AC AAF15665;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:100.  
XX  
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200055174-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005988.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
PI Rosen CA, Ruben SM;  
XX  
XX WPI; 2000-587513/55.  
DR P-PSDB; AAB56462.  
XX  
PT Prostate cancer associated gene sequences, referred to as prostate cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as prostate cancer.  
XX  
PS Claim 1; Page 679-680; 2338pp; English.  
XX  
CC AAF15566 to AAF15505 encode the human prostate cancer associated  
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
CC The prostate cancer antigens can have neuroprotective, cytostatic,  
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
CC and can be used in gene therapy. The prostate cancer antigen  
CC polynucleotides may be used for detection of prostate cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The prostate cancer antigens may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,

CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention

XX SQ Sequence 599 BP; 163 A; 169 C; 139 G; 120 T; 0 U; 8 Other;

Query Match 80.4%; Score 111; DB 3; Length 599;  
 Best Local Similarity 99.2%; Pred. No. 1.5e-22;  
 Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 16 TCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCACGCCCGCG 75

Db 14 TCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCACGCCCGCG 73

Qy 76 CGCCAGCCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTGT 135

Db 74 CGCCA-CCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTGT 132

Qy 136 CCC 138

Db 133 CCC 135

Search completed: April 26, 2004, 14:04:43  
 Job time : 276 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 2161 Seconds  
(without alignments)  
1906.979 Million cell updates/sec

Title: US-09-645-590-1

Perfect score: 138

Sequence: 1 acccattcgctgctctca.....actgacctcgccctgtccc 138

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_esti.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_pbg.\*

27: em\_gss\_vrl.\*

28: gb\_gssi.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	463	14	CA772698 1083g01.y
2	138	100.0	584	12	BI457963 603198956
3	138	100.0	873	13	BU930481 AGENCOURT
4	137	99.3	300	9	AU100303 AU100303

5	135	97.8	136	9	AU077324
6	128	92.8	521	9	AI879081
7	127	92.0	556	13	BQ721485
8	127	92.0	557	13	BQ925183
9	127	92.0	963	13	BQ876913
10	126.4	91.6	550	9	AI928896
11	125.4	90.9	544	9	AI826374
12	125	90.6	468	13	BI101548
13	124	89.9	433	9	AI929147
14	114	82.6	567	13	BQ932266
15	106.8	77.4	1123	13	BQ86097
16	87	63.0	766	13	BU930120
17	86.6	62.8	1695	10	BF680552
18	80	58.0	498	9	AI199681
19	71	51.4	424	9	AA061961
20	71	51.4	443	9	AI385504
21	71	51.4	492	13	BX527459
22	71	51.4	556	11	AK002982
23	71	51.4	585	13	BU937569
24	71	51.4	591	13	BU558492
25	71	51.4	600	13	BU604192
26	71	51.4	926	13	BU936355
27	69.6	50.4	489	10	BE653651
28	69.6	50.4	493	13	BQ84972
29	69.6	50.4	534	13	BQ084688
30	69.6	50.4	569	13	BQ564644
31	68.4	49.6	574	9	AI198311
32	66.2	48.0	435	14	CB792893
33	63.2	45.8	402	14	CB769232
34	63.2	45.8	520	12	BQ644605
35	63.2	45.8	529	14	CB719328
36	63.2	45.8	544	14	CB612099
37	63.2	45.8	587	14	CB585333
38	63	45.7	408	9	AA270394
39	63	45.7	483	14	W70782
40	62.2	45.1	570	12	BQ44605
41	61.6	44.6	364	13	BQ290146
42	56.6	41.0	454	14	CB741987
43	56.6	41.0	461	14	CB736748
44	56.6	41.0	499	14	CB712314
45	56.6	41.0	500	14	CB712006

## ALIGNMENTS

RESULT 1

CA772698

LOCUS

DEFINITION

CA772698 463 bp mRNA linear EST 03-DEC-2002  
1083g01.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6133056 5',  
similar to SW:NEUY\_HUMAN P01303 NEUROPEPTIDE Y PRECURSOR ;, mRNA  
sequence.

CA772698

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA772698 463 bp mRNA linear EST 03-DEC-2002  
1083g01.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6133056 5',  
similar to SW:NEUY\_HUMAN P01303 NEUROPEPTIDE Y PRECURSOR ;, mRNA  
sequence.  
CA772698 GI:26009965  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 463)  
Mellon, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
Lemshka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,  
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,  
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,  
Williams, T., Jackson, Y. and Bowers, Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Other ESTs: i083g01.x1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)

Putative full length read  
vector to vector length is 598

Seq primer: -40RP from Gibco.

Location/Qualifiers

FEATURES  
source

1. 463

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6133056"

/tissue\_type="Purified pancreatic islet"

/lab\_host="DH10B"

/clone\_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
Size-selected on agarose gel. Average insert size ~1kb. 5'  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permutt Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 138; DB 14; Length 463;

Best Local Similarity 100.0%; Pred. No. 2e-24; 0; Indels 0; Gaps 0;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGCCGC 60

Db 28 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGCCGC 87

QY 61 CCAGCCAGCCCGCGCGGCGAGCACCACATCTAGTAAACAAGCGACTGGGGCTGTCGGAC 120

Db 88 CCAGCCAGCCCGCGCGGCGAGCACCACATCTAGTAAACAAGCGACTGGGGCTGTCGGAC 147

QY 121 TCACCTCGCCCTGTCCC 138

Db 148 TCACCTCGCCCTGTCCC 165

RESULT 2

BI457963

LOCUS

DEFINITION BI457963 584 bp mRNA linear EST 21-AUG-2001

ACCESSION 603198956F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5278692 5',

VERSION mRNA sequence.

KEYWORDS BI457963.1 GI:15248619

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE 1 (bases 1 to 584)

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LLAM11703 row: 0 column: 13

High quality sequence stop: 584.

FEATURES  
source

Location/Qualifiers

1. 584

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5278692"

/tissue\_type="hypothalamus"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_96"

/note="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
(gtcgag); Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to 500. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NHGRI/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

ORIGIN

Query Match 100.0%; Score 138; DB 12; Length 584;

Best Local Similarity 100.0%; Pred. No. 2.2e-24;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGCCGC 60

Db 8 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGCCGC 67

QY 61 CCAGCCAGCCCGCGCGGCGAGCACCACATCTAGTAAACAAGCGACTGGGGCTGTCGGAC 120

Db 68 CCAGCCAGCCCGCGCGGCGAGCACCACATCTAGTAAACAAGCGACTGGGGCTGTCGGAC 127

QY 121 TCACCTCGCCCTGTCCC 138

Db 128 TCACCTCGCCCTGTCCC 145

RESULT 3

BU930481

LOCUS

DEFINITION BU930481 873 bp mRNA linear EST 18-OCT-2002

ACCESSION AGENCOURT 10424773 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:6668512

VERSION 5', mRNA sequence.

KEYWORDS BU930481 GI:24119300

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE 1 (bases 1 to 873)

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: CLONTECH

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2942 row: 1 column: 16

High quality sequence stop: 510.

Location/Qualifiers

1. 873

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"



```

/clone="IMAGE:6668512"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: Sfii (ggcccttcggcc); Site 2: Sfii
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGGC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

## ORIGIN

```

Query Match      100.0%; Score 138; DB 13; Length 873;
Best Local Similarity 100.0%; Pred. No. 2.4e-24;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60
Db 4 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 63

QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
Db 64 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 123

QY 121 TGACCCCTCGCCCTGTCTCC 138
Db 124 TGACCCCTCGCCCTGTCTCC 141
```

## RESULT 4

```

AUI00303
LOCUS          300 bp mRNA linear EST 05-APR-2001
DEFINITION    Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
Zrv6c665 similar to Human neurotrophin Y (NPY) mRNA, mRNA sequence.
ACCESSION    AUI00303
VERSION      AUI00303.1 GI:13551432
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J.,
AUTHORS      Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S.,
Okubo,K., Sugama,A. and Sugano S.
In silico mapping of the 5'-ends of human mRNAs using full-length
enriched and 5'-end enriched cDNA libraries constructed by
Oligo-capping method
Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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## TITLE

## JOURNAL

## COMMENT

## FEATURES

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1..136
/organism="Homo sapiens"
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Query Match      97.8%; Score 135; DB 9; Length 136;
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Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60
Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60

QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120

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## FEATURES

source

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## ORIGIN

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Best Local Similarity 99.3%; Pred. No. 3.2e-24;
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Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60
Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60

QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120

QY 121 TGACCCCTCGCCCTGTCTCC 138
Db 121 TGACCCCTCGCCCTGTCTCC 138
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## RESULT 5

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AUI077324
LOCUS          136 bp mRNA linear EST 04-MAY-2000
DEFINITION    Sugano cDNA library Homo sapiens cDNA clone Zrv6c665
similar to 5'-end region of Human neurotrophin Y (NPY) mRNA, mRNA
sequence.
ACCESSION    AUI077324
VERSION      AUI077324.1 GI:7440000
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Suzuki,Y., Ishihara,D., Sasaki,M., Nakagawa,H., Hata,H.,
AUTHORS      Tsunoda,T., Watanabe,M., Komatsu,T., Ota,T., Isogai,T., Suyama,A.
and Sugano,S.
Statistical analysis of the 5' untranslated region of human mRNA
using 'Oligo-Capped' cDNA libraries
Genomics 64 (3), 286-297 (2000)
2021373
10756096
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
This clone was obtained from a '5'-end-enriched' cDNA library
constructed by 'Oligo-Capping' method. The coding region starts
from the 50 bp upstream to the 3'-end.
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## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## FEATURES

source

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1..136
/organism="Homo sapiens"
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## ORIGIN

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Query Match      97.8%; Score 135; DB 9; Length 136;
Best Local Similarity 99.3%; Pred. No. 8.1e-24;
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60
Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60

QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120

QY 121 TGACCCCTCGCCCTGTCTCC 136
Db 121 TGACCCCTCGCCCTGTCTCC 136
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RESULT 6
LOCUS      AI879081               521 bp      mRNA      linear      EST 23-AUG-1999
DEFINITION au54b11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2518557 5', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION  AI879081
VERSION     AI879081.1      GI:5553130
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 521)
AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
TITLE     WashU-NCI human EST Project
JOURNAL   Unpublished (1997)
COMMENT   Other ESTs: au54b11.x1
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 425.
FEATURES   Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2518557"
                /sex="male"
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                /dev_stage="5 months post-conception"
                /lab_host="DH10B"
                /clone_lib="Schneider fetal brain 00004"
                /note="Organ: brain; Vector: pBluescript SK (Stratagene);
                Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was
                prepared from human fetal brain tissue. 5' and 3'
                adaptors were used in cloning as follows: 5' adaptor
                sequence:
                5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAATTAATCCCCCCCCCCC-3'
                and 3' adaptor sequence:
                5'-GAGAGAGAGACTCGAGTTTCTTTTCTTTTCTTTT-3'. The library was
                size-selected for >0.5 kb inserts and has an average
                insert size estimated at 1.2 kb. This library was
                constructed using the CAP-trapper method for full-length
                enrichment and has not undergone amplification. Library
                was constructed by Dr. Claudio Schneider (LNCIB-Area
                Science Park, Trieste, Italy)."
ORIGIN
Query Match      92.8%; Score 128; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 6.5e-22;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CTGGCTCTCACCCCTCGAGACGCTCGCCCGACAGCATAGTACTTGGCCGCCAGCCAGC 70
      |||
Db 1 CTGGCTCTCACCCCTCGAGACGCTCGCCCGACAGCATAGTACTTGGCCGCCAGCCAGC 60

Qy 71 CCGCGCGCCAGCCACCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGACTGACCCCTGC 130
      |||
Db 61 CCGCGCGCCAGCCACCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGACTGACCCCTGC 120

Qy 131 CTGTGCC 138
      |||
      121 CTGTGCC 127

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Db 121 CCTGTCCC 128
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      121 CCTGTCCC 128

RESULT 7
LOCUS      BQ721485               556 bp      mRNA      linear      EST 16-JUL-2002
DEFINITION AGENCOURT 8234409 Lupski sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6188546 5', mRNA sequence.
ACCESSION  BQ721485
VERSION     BQ721485.1      GI:21860382
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 556)
AUTHORS   NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
            Email: cgapbe-r@mail.nih.gov
COMMENT   Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Cloning by: Agencourt Bioscience Corporation
            Cloning distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM3584 row: f column: 03
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                /clone_lib="Lupski sympathetic trunk"
                /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
                NotI; Site 2: SalI; cDNA made by oligo-dT priming.
                Directionally cloned using the following adaptors:
                5'-TCGACCCAGCGGCTCCG-3' and
                5'-GACTAGTCTAGTCGCGCGCGCCT(15)-3'. Size selected >
                1 kb for average insert length 1.9 kb. This is a primary
                library, non-amplified. Library constructed by Life
                Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                College of Medicine); available through Life
                Technologies."
ORIGIN
Query Match      92.0%; Score 127; DB 13; Length 556;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCCGCCAGCCAGCC 71
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Db 1 TGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCCGCCAGCCAGCC 60

Qy 72 CGCGCGCCAGCCACCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGACTGACCCCTGCC 131
      |||
Db 61 CGCGCGCCAGCCACCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGACTGACCCCTGCC 120

Qy 132 CTGTCCC 138
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      121 CTGTCCC 127

RESULT 8
BQ25183

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LOCUS B0925183 557 bp mRNA linear EST 20-AUG-2002  
 DEFINITION AGENCOURT\_8821446 Lupski\_sciatic nerve Homo sapiens cDNA clone  
 IMAGE:6203754 5', mRNA sequence.  
 ACCESSION B0925183  
 VERSION B0925183.1 GI:22340214  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 557)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM13623 row: 0 column: 19  
 High quality sequence stop: 556.  
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 Directionally cloned using the following adaptors:  
 5'-TCGACCCACCGCTCCG-3' and  
 5'-GACTAGTCTAGATCGCGAGCGCGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.87 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

ORIGIN  
 Query Match 92.0%; Score 127; DB 13; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-21;  
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 71  
 Db 1 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 60  
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 Db 61 CGCGCGCCAGCCACCATGCTAGGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 120  
 QY 132 CTGTCCC 138  
 Db 121 CTGTCCC 127  
 RESULT 9  
 LOCUS B0876913 963 bp mRNA linear EST 16-AUG-2002  
 DEFINITION AGENCOURT\_8417678 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone  
 IMAGE:6193004 5', mRNA sequence.  
 ACCESSION B0876913  
 VERSION B0876913.1 GI:22268921  
 KEYWORDS EST.

LOCUS B0925183 557 bp mRNA linear EST 20-AUG-2002  
 DEFINITION AGENCOURT\_8821446 Lupski\_sciatic nerve Homo sapiens cDNA clone  
 IMAGE:6203754 5', mRNA sequence.  
 ACCESSION B0925183  
 VERSION B0925183.1 GI:22340214  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 557)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM13623 row: 0 column: 19  
 High quality sequence stop: 556.  
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 /clone="IMAGE:6203754"  
 /sex="male"  
 /tissue\_type="sciatic nerve"  
 /dev\_stage="adult, 70 yr"  
 /lab\_host="DH10B"  
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 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
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 Directionally cloned using the following adaptors:  
 5'-TCGACCCACCGCTCCG-3' and  
 5'-GACTAGTCTAGATCGCGAGCGCGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.87 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

ORIGIN  
 Query Match 92.0%; Score 127; DB 13; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-21;  
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 QY 12 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 71  
 Db 1 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 60  
 QY 72 CGCGCGCCAGCCACCATGCTAGGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 131  
 Db 61 CGCGCGCCAGCCACCATGCTAGGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 120  
 QY 132 CTGTCCC 138  
 Db 121 CTGTCCC 127  
 RESULT 9  
 LOCUS B0876913 963 bp mRNA linear EST 16-AUG-2002  
 DEFINITION AGENCOURT\_8417678 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone  
 IMAGE:6193004 5', mRNA sequence.  
 ACCESSION B0876913  
 VERSION B0876913.1 GI:22268921  
 KEYWORDS EST.

LOCUS B0925183 557 bp mRNA linear EST 20-AUG-2002  
 DEFINITION AGENCOURT\_8821446 Lupski\_sciatic nerve Homo sapiens cDNA clone  
 IMAGE:6203754 5', mRNA sequence.  
 ACCESSION B0925183  
 VERSION B0925183.1 GI:22340214  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 557)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM13595 row: 0 column: 21  
 High quality sequence stop: 517.  
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 /sex="male"  
 /tissue\_type="sympathetic trunk"  
 /dev\_stage="adult, 16 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski sympathetic trunk"  
 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACCGCTCCG-3' and  
 5'-GACTAGTCTAGATCGCGAGCGCGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 1.4e-21;  
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 Db 1 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 60  
 QY 72 CGCGCGCCAGCCACCATGCTAGGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 131  
 Db 61 CGCGCGCCAGCCACCATGCTAGGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 120  
 QY 132 CTGTCCC 138  
 Db 121 CTGTCCC 127  
 RESULT 10  
 LOCUS AI928896/c 550 bp mRNA linear EST 23-AUG-1999  
 DEFINITION au5f07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone  
 IMAGE:2519653 3', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR  
 (HUMAN); mRNA sequence.  
 ACCESSION AI928896  
 VERSION AI928896.1 GI:5664860  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 550)

**AUTHORS**  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, F., Wyllie, F., Waterston, R. and Wilson, R.  
**TITLE**  
 WashU-NCI human EST project  
**JOURNAL**  
 Unpublished (1997)  
**COMMENT**  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 481.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2519653"  
 /sex="male"  
 /tissue type="frontal lobe"  
 /dev stage="5 months post-conception"  
 /lab\_host="DH10B"  
 /clone\_lib="Schneider fetal brain 00004"  
 /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site 1: SSTI; Site 2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:  
 5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAATTAATCCCGCCCCCCC-3' and 3' adaptor sequence:  
 5'-GAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."  
**FEATURES**  
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 /sex="male"  
 /tissue type="frontal lobe"  
 /dev stage="5 months post-conception"  
 /lab\_host="DH10B"  
 /clone\_lib="Schneider fetal brain 00004"  
 /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site 1: SSTI; Site 2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:  
 5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAATTAATCCCGCCCCCCC-3' and 3' adaptor sequence:  
 5'-GAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."  
**ORIGIN**  
 Query Match 91.6%; Score 126.4; DB 9; Length 550;  
 Best Local Similarity 97.7%; Pred. No. 1.7e-21;  
 Matches 127; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 9 CGCTGGCTTCAACCCCTCGAGACGCTGCGCCGACGAGCATAGTACTTGGCCGCCAGCCAC 68  
 Db |||||  
 550 CGNTGGCTTCAACCCNTCGGAGACGCTGCGCCGACGAGCATAGTACTTGGCCGCCAGCCAC 491  
 QY 69 GCCCGCGCCAGCCACCAGTCTAGGTAAACAGCGACTGGGCTGTGCGGACTGACCCCTC 128  
 Db |||||  
 490 GCCCGCGCCAGCCAGCCACCAGTCTAGGTAAACAGCGACTGGGCTGTGCGGACTGACCCCTC 431  
 QY 129 GCCCTGTGCC 138  
 Db |||||  
 430 GCCCTGTGCC 421  
**RESULT 11**  
 AI826374/c  
 LOCUS  
 DEFINITION  
 wk44q12.x1 NCI CGAP pr22 Homo sapiens cDNA clone IMAGE:2418310 3' similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR (HUMAN);, mRNA  
 sequence.  
 AI826374  
 AI826374.1 GI:5447045  
 VERSION  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS**  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, F., Wyllie, F., Waterston, R. and Wilson, R.  
**TITLE**  
 WashU-NCI human EST project  
**JOURNAL**  
 Unpublished (1997)  
**COMMENT**  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 481.  
 Location/Qualifiers  
 1..550  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2519653"  
 /sex="male"  
 /tissue type="frontal lobe"  
 /dev stage="5 months post-conception"  
 /lab\_host="DH10B"  
 /clone\_lib="Schneider fetal brain 00004"  
 /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site 1: SSTI; Site 2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:  
 5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAATTAATCCCGCCCCCCC-3' and 3' adaptor sequence:  
 5'-GAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."  
**FEATURES**  
 source  
 1..550  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2519653"  
 /sex="male"  
 /tissue type="frontal lobe"  
 /dev stage="5 months post-conception"  
 /lab\_host="DH10B"  
 /clone\_lib="Schneider fetal brain 00004"  
 /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site 1: SSTI; Site 2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:  
 5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAATTAATCCCGCCCCCCC-3' and 3' adaptor sequence:  
 5'-GAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."  
**ORIGIN**  
 Query Match 91.6%; Score 126.4; DB 9; Length 550;  
 Best Local Similarity 97.7%; Pred. No. 1.7e-21;  
 Matches 127; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 9 CGCTGGCTTCAACCCCTCGAGACGCTGCGCCGACGAGCATAGTACTTGGCCGCCAGCCAC 68  
 Db |||||  
 550 CGNTGGCTTCAACCCNTCGGAGACGCTGCGCCGACGAGCATAGTACTTGGCCGCCAGCCAC 491  
 QY 69 GCCCGCGCCAGCCACCAGTCTAGGTAAACAGCGACTGGGCTGTGCGGACTGACCCCTC 128  
 Db |||||  
 490 GCCCGCGCCAGCCAGCCACCAGTCTAGGTAAACAGCGACTGGGCTGTGCGGACTGACCCCTC 431  
 QY 129 GCCCTGTGCC 138  
 Db |||||  
 430 GCCCTGTGCC 421  
**RESULT 12**  
 BX101548  
 LOCUS  
 DEFINITION  
 clone IMAGE:1894398, mRNA sequence.  
 BX101548  
 BX101548.1 GI:27844953  
 VERSION  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
 1 (bases 1 to 468)  
**AUTHORS**  
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, B., Peters, M., Radelof, U., Schneider, D. and Korn, B.  
**TITLE**  
 Human Unigeneset - RZPD3  
**JOURNAL**  
 Unpublished (2003)  
**COMMENT**  
 Contact: Ina Rolfes

**REFERENCE**  
 1 (bases 1 to 544)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
**AUTHORS**  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
**JOURNAL**  
 Unpublished (1997)  
**COMMENT**  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html  
 Insert Length: 490 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 461.  
 Location/Qualifiers  
 1..544  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2418310"  
 /sex="male"  
 /tissue type="normal prostate"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr22"  
 /note="Organ: prostate; Vector: pWT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pWT3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."  
**FEATURES**  
 source  
 1..544  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2418310"  
 /sex="male"  
 /tissue type="normal prostate"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr22"  
 /note="Organ: prostate; Vector: pWT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pWT3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."  
**ORIGIN**  
 Query Match 90.9%; Score 125.4; DB 9; Length 544;  
 Best Local Similarity 99.2%; Pred. No. 2.9e-21;  
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 TGGCTTCAACCCCTCGAGACGCTGCGCCGACGAGCATAGTACTTGGCCGCCAGCCAGCC 71  
 Db |||||  
 544 TGGCTTCAACCCCTCGAGACGCTGCGCCGACGAGCATAGTACTTGGCCGCCAGCCAGCC 485  
 QY 72 CGCGCGCCAGCCACCAGTCTAGGTAAACAGCGACTGGGCTGTGCGGACTGACCCCTCGCC 131  
 Db |||||  
 484 CGCGCGCCAGCCACCAGTCTAGGTAAACAGCGACTGGGCTGTGCGGACTGACCCCTCGCC 425  
 QY 132 CTGTGCC 138  
 Db |||||  
 424 CTGTGCC 418  
**RESULT 12**  
 BX101548  
 LOCUS  
 DEFINITION  
 clone IMAGE:1894398, mRNA sequence.  
 BX101548  
 BX101548.1 GI:27844953  
 VERSION  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
 1 (bases 1 to 468)  
**AUTHORS**  
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, B., Peters, M., Radelof, U., Schneider, D. and Korn, B.  
**TITLE**  
 Human Unigeneset - RZPD3  
**JOURNAL**  
 Unpublished (2003)  
**COMMENT**  
 Contact: Ina Rolfes

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGP998K074642.  
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfes  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)

This clone is available royalty-free from RZPD;  
contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
M13r, Primer sequence: TTTCACAGAAACAGCTATGAC.

## FEATURES

source

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1. .468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP998K074642 ; IMAGE:1894398"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta 8to9weeks 2NBP8to9w"
/notes="Organ: placenta; Vector: p77T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATGCTGAAGTCGGAGCGCGCGATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p77T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaudo."
```

## ORIGIN

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Query Match          90.6%; Score 125; DB 13; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 73
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 60

QY 74 CGCGCCAGCCACCATGTAGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCT 133
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CGCGCCAGCCACCATGTAGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCT 120

QY 134 GTCCC 138
| | | | |
Db 121 GTCCC 125
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RESULT 13
AI929147
LOCUS
DEFINITION
au65f07.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
(HUMAN); mRNA sequence.
AI929147
VERSION
AI929147.1 GI:5665111
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 433)
AUTHORS
Hallier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Krizman D., Kucaba F., Lacy M., Le N., Lennon G., Marra M.,
Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
Theising B., White Y., Wylie T., Waterston R. and Wilson R.
WashU-NCI human EST Project
Unpublished (1997)
```

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40RP from Gibco.

## FEATURES

source

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1. .433
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2519653"
/sex="male"
/tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
/clone_lib="Schneider fetal brain 00004"
/notes="Organ: brain; Vector: pBluescript SK (Stratagene);
Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence:
5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAAATATCCGCCGCCGCC-3'
and 3' adaptor sequence:
5'-GAGAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was
size-selected for >0.5 kb inserts and has an average
insert size estimated at 1.2 kb. This library was
constructed using the CAP-trapper method for full-length
enrichment and has not undergone amplification. Library
was constructed by Dr. Claudio Schneider (LNCIB-Area
Science Park, Trieste, Italy)."
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## ORIGIN

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Query Match          89.9%; Score 124; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.2e-21;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 74
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 CTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 60

QY 75 GCGCCAGCCACCATGTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTG 134
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GCGCCAGCCACCATGTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTG 120

QY 135 TCCC 138
| | | | |
Db 121 TCCC 124
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## RESULT 14

BQ932266

LOCUS

DEFINITION

AGENCOURT 8804926 Lupski sciatic nerve Homo sapiens cDNA clone

IMAGE:6197017 5', mRNA sequence.

BQ932266

ACCESSION

VERSION

BQ932266.1 GI:22347297

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 567)

AUTHORS

NIH-MGC <http://imgc.ncbi.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM13606 row: g column: 02  
High quality sequence stop: 566.

FEATURES  
source

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/sex="male"  
/tissue\_type="sciatic nerve"  
/dev\_stage="adult, 70 yr"  
/lab\_host="DH10B"  
/clone\_lib="Lupski sciatic nerve"  
/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCACGGTCCG-3' and  
5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.87 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

ORIGIN

Query Match 82.6%; Score 114; DB 13; Length 567;  
Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 25 TCGAGAGCGCTCCGCGACAGCATAGTACTTCGCGCCCGACGCGCGCGCCAGCCA 84  
Db 1 TCGGAGAGCGCTCCGCGCGACAGCATAGTACTTCGCGCCCGACGCGCGCGCCAGCCA 60  
  
QY 85 CCATGCTAGGTAAAGAGCGTGGGGCTGTCGGAGTACCTGACCTGCGCCGTGCC 138  
Db 61 CCATGCTAGGTAAAGAGCGTGGGGCTGTCGGAGTACCTGACCTGCGCCGTGCC 114

RESULT 15  
BQ886097

LOCUS BQ886097 1123 bp mRNA linear EST 16-AUG-2002  
DEFINITION AGENCOURT 8673508 Lupski\_sciatic\_nerve Homo sapiens cDNA clone  
IMAGE:6199943 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BQ886097.1 GI:22278111  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1123)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

REFERENCE

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM13613 row: p column: 24  
High quality sequence start: 90  
High quality sequence stop: 266.

FEATURES  
source

1. .1123  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6199943"  
/sex="male"  
/tissue\_type="sciatic nerve"  
/dev\_stage="adult, 70 yr"  
/lab\_host="DH10B"  
/clone\_lib="Lupski sciatic nerve"  
/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCACGGTCCG-3' and  
5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.87 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

ORIGIN

Query Match 77.4%; Score 106.8; DB 13; Length 1123;  
Best Local Similarity 90.6%; Pred. No. 1.6e-16;  
Matches 125; Conservative 0; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGAGCGTGGCCGCGACAGATAGTACTTCCCGC 60  
Db 41 ACCGCGCCAGCGTCCGCTCACCCCTCGGAGAGCGTGGCCGCGACAG-ATTGTACTCGACGC 99  
  
QY 61 CCAGCGACGCGCGCGCGCGCGCCATGCTAGGTAAAGAGCGTGGGGCTGTCGGGAC 120  
Db 100 CCAGCGACGCGCGCGCGCGCCATGCTAGGTAAAGAGCGTGGGGCTGTCGGGAC 159  
  
QY 121 TGACCCCTGCGCCCTGTCCC 138  
Db 160 TGACCCCTGCGCCCTGTCCC 177

Search completed: April 26, 2004, 15:45:52  
Job time : 2165 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 59.5 Seconds  
(without alignments)  
1287.113 Million cell updates/sec

Title: US-09-645-590-1  
Perfect score: 138  
Sequence: 1 accccatccgctggctctca.....actgacccctgcctctgtccc 138

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	551	3	US-08-994-946A-5
2	138	100.0	551	4	US-09-291-994-5
3	136.4	98.8	1588	4	US-09-976-594-625
4	113.2	82.0	122	4	US-09-621-976-8234
5	91	65.9	325	3	US-08-934-946A-1
6	91	65.9	325	4	US-09-291-994-1
7	52	37.7	247	3	US-08-994-946A-2
8	52	37.7	247	4	US-09-291-994-2
9	30.6	22.2	945	4	US-09-252-991A-14797
10	30.6	22.2	2550	4	US-09-252-991A-14954
11	30.2	21.9	1242	4	US-09-352-991A-9668
12	30.2	21.9	1518	4	US-09-489-039A-6357
13	30.2	21.9	1521	4	US-09-252-991A-9746
14	30.2	21.9	2511	4	US-09-252-991A-9494
15	30.2	21.9	2583	4	US-09-252-991A-9541
16	29.6	21.4	588	4	US-09-252-991A-6523
17	29.6	21.4	891	4	US-09-352-991A-6513
18	29.6	21.4	999	4	US-09-252-991A-14871
19	29.6	21.4	1608	4	US-09-252-991A-14491
20	29.2	21.2	670	4	US-09-009-816-3
21	29.2	21.2	1104	4	US-09-009-816-1
22	29.2	21.2	1108	4	US-09-800-729-42
23	29.2	21.2	1141	4	US-09-800-729-78
24	29.2	21.2	1237	4	US-09-800-729-80
25	28.8	20.9	2748	4	US-09-489-039A-1078
26	28.4	20.6	1247	1	US-08-278-729A-32
27	28.4	20.6	1247	1	US-08-155-343A-32

28	28.4	20.6	1247	1	US-08-406-672-32	Sequence 32, Appl
29	28.4	20.6	1247	1	US-08-643-563A-32	Sequence 32, Appl
30	28.4	20.6	1247	1	US-08-643-763A-32	Sequence 32, Appl
31	28.4	20.6	1247	1	US-08-462-623-32	Sequence 32, Appl
32	28.4	20.6	1247	1	US-08-451-953A-32	Sequence 32, Appl
33	28.4	20.6	1247	2	US-08-445-468A-32	Sequence 32, Appl
34	28.4	20.6	1247	2	US-08-461-397A-32	Sequence 32, Appl
35	28.4	20.6	1247	3	US-08-912-088-32	Sequence 32, Appl
36	28.4	20.6	1247	3	US-08-278-730A-32	Sequence 32, Appl
37	28.4	20.6	1247	3	US-08-445-467-32	Sequence 32, Appl
38	28.4	20.6	1247	3	US-08-480-515A-32	Sequence 32, Appl
39	28.4	20.6	1247	4	US-09-170-936-32	Sequence 32, Appl
40	28.4	20.6	1247	4	US-08-461-113-32	Sequence 32, Appl
41	28.4	20.6	1247	4	US-08-456-033-32	Sequence 32, Appl
42	28.4	20.6	1247	4	US-08-643-321-30	Sequence 32, Appl
43	28.4	20.6	1247	5	PCT-US93-07190-32	Sequence 30, Appl
44	28.4	20.6	1247	5	PCT-US93-07231-32	Sequence 32, Appl
45	28.4	20.6	1247	5	PCT-US93-08742-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-08-994-946A-5  
; Sequence 5, Application US/08994946A  
; Patent No. 6046317  
; GENERAL INFORMATION:

APPLICANT: Koulou, Markku  
APPLICANT: Karvonen, Matti  
APPLICANT: Pesonen, Ullamari  
APPLICANT: Uusitupa, Matti  
TITLE OF INVENTION: A DNA Molecule Encoding a Mutant  
Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses  
TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.  
STREET: 555 13th Street NW, Suite 701-E  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/994,946A  
FILING DATE: 19-DEC-1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 2328-110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-783-6040  
TELEFAX: 202-783-6031  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 551 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 87..170  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 87..377  
US-08-994-946A-5





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Db      121 TG 122
||
RESULT 5
US-08-994-946A-1
; Sequence 1, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-994-946A-1

Query Match      65.9%; Score 91; DB 3; Length 325;
Best Local Similarity 90.7%; Pred. No. 2.6e-18;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 60
Db      210 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 269

QY      61 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTAAACAGCGACTG 107
Db      270 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTAAACAGCGACTG 316

RESULT 7
US-08-994-946A-2
; Sequence 2, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-994-946A-1

Query Match      65.9%; Score 91; DB 3; Length 325;
Best Local Similarity 90.7%; Pred. No. 2.6e-18;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 60
Db      210 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 269

QY      61 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTAAACAGCGACTG 107
Db      270 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTAAACAGCGACTG 316

RESULT 6
US-09-291-994-1
; Sequence 1, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine

```

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 87 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACCTCGCCCTGTCCTCC 138  
Db 30 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACCTCGCCCTGTCCTCC 81

## RESULT 8

US-09-291-994-2  
; Sequence 2, Application US/09291994  
; Patent No. 6312898  
; GENERAL INFORMATION:  
; APPLICANT: Koulou, Markku  
; APPLICANT: Karvonen, Matti  
; APPLICANT: Pesonen, Ullamari  
; APPLICANT: Uusitupa, Matti  
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing  
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine  
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide  
; TITLE OF INVENTION: Y Gene.  
; FILE REFERENCE: 2328-112.A  
; CURRENT APPLICATION NUMBER: US/09/291,994  
; CURRENT FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-291-994-2

Query Match 37.7%; Score 52; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07; Indels 0; Gaps 0;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 87 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACCTCGCCCTGTCCTCC 138  
Db 30 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACCTCGCCCTGTCCTCC 81

## RESULT 9

US-09-252-991A-14797/c  
; Sequence 14797, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14797  
; LENGTH: 945  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14797

Query Match 22.2%; Score 30.6; DB 4; Length 945;  
Best Local Similarity 51.9%; Pred. No. 2.1; Indels 0; Gaps 0;  
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGAGCATAGTACTTGGCCG 60  
Db 611 ACCCCGGGGTGGCAACCGAGAGAGCTTGACGATCGCCCGCTGCGCTCGCCGAGCATC 552  
QY 61 CAGCCACGCGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 120  
Db 551 GCCGGCAGCGCGCTCGGCAACCAACAGGTGGGAGCAGCGAACCCCGAGCTCGGCC 492

QY 121 TGACCTCGCCCT 133  
Db 491 TCAATCTCGTCT 479

## RESULT 10

US-09-252-991A-14954  
; Sequence 14954, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14954  
; LENGTH: 2550  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14954

Query Match 22.2%; Score 30.6; DB 4; Length 2550;  
Best Local Similarity 51.9%; Pred. No. 2.4; Indels 0; Gaps 0;  
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGAGCATAGTACTTGGCCG 60  
Db 1890 ACCCCGGGGTGGCAACCGAGAGCTTGACGATCGCCCGCTGCGCTCGCCGAGCATC 1939  
QY 61 CAGCCACGCGCGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 120  
Db 1940 GCCGGCAGCGCGCTCGGCAACCAACAGGTGGGAGCAGCGAACCCCGAGCTCGGCC 1999  
QY 121 TGACCTCGCCCT 133  
Db 2000 TCAATCTCGTCT 2012

## RESULT 11

US-09-252-991A-9668/c  
; Sequence 9668, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9668  
; LENGTH: 1242  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9668

Query Match 21.9%; Score 30.2; DB 4; Length 1242;  
Best Local Similarity 53.9%; Pred. No. 2.8; Indels 0; Gaps 0;  
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
QY 24 CTCGGAGAGCTCGCCGACGAGCATAGTACTTGGCCGACGAGCCAGCCGCGCGCCAGCC 83

Db 947 CTCGAGAGCCCGCCAGACGGCTCTCGATATGGCCAGCGCCGCGCCAGCTTCCTGGCC 888

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTCTCCGAGACTGACCTTCGCCCTGTGCC 138

Db 887 AACATGAGCCACGAGATCCGACGCCGCTGAACGCCCTGCTCGCATGCTCTCGC 833

## RESULT 12

US-09-489-039A-6357/c  
; Sequence 6357, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 6357  
; LENGTH: 1518  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-6357

Query Match 21.9%; Score 30.2; DB 4; Length 1518;  
Best Local Similarity 60.2%; Pred. No. 2.9;  
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2 CCCCATCCGCTGCTCTCACCCCTCGAGAGCGTCCGCCGACAGCATAGTACTTGGCGCC 61

Db 1056 CCCCATCAGCTCGTTCATCCAGCGCGACCCCGCGCAAAAGCGCTGAGCTTGCTTT 997

QY 62 CAGCCAGCGCCGCGCGCCAGCCA 84

Db 996 CAGCAGGCCAGTACCGCATCCA 974

## RESULT 13

US-09-252-991A-9746/c  
; Sequence 9746, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9746  
; LENGTH: 1521  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9746

Query Match 21.9%; Score 30.2; DB 4; Length 1521;  
Best Local Similarity 53.9%; Pred. No. 2.9;  
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 24 CTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCGACAGCCAGCCGCGCGCCAGCC 83

Db 1506 CTCGAGAGAGCCCGCCAGACCGCTCTCGATATGCGCCGCGCGCCAGCTTCCTGGCC 1447

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTCTCGGAGCTGACCTTCGCCCTGTGCC 138

Db 1446 AACATGAGCCACGAGATCCGACGCCGCTGAACGGCTGTCTCGGCATGCTCTCGC 1392

## RESULT 14

US-09-252-991A-9494  
; Sequence 9494, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9494  
; LENGTH: 2511  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9494

Query Match 21.9%; Score 30.2; DB 4; Length 2511;  
Best Local Similarity 53.9%; Pred. No. 3.1;  
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 24 CTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCGACAGCCAGCCGCGCGCCAGCC 83

Db 932 CTCGAGAGAGCCCGCCAGACCGCTCTCGATATGCGCCGCGCGCCAGCTTCCTGGCC 991

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAGCTGACCTTCGCCCTGTGCC 138

Db 992 AACATGAGCCACGAGATCCGACGCCGCTGAACGGCTGTCTCGGCATGCTCTCGC 1046

## RESULT 15

US-09-252-991A-9541  
; Sequence 9541, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9541  
; LENGTH: 2583  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9541

Query Match 21.9%; Score 30.2; DB 4; Length 2583;  
Best Local Similarity 53.9%; Pred. No. 3.1;  
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 24 CTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCGACAGCCAGCCGCGCGCCAGCC 83

Db 1096 CTCGAGAGAGCCCGCCAGACCGCTCTCGATATGCGCCGCGCGCCAGCTTCCTGGCC 1155

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAGCTGACCTTCGCCCTGTGCC 138

Db 1156 AACATGAGCCACGAGATCCGACGCCGCTGAACGGCTGTCTCGGCATGCTCTCGC 1210

Search completed: April 26, 2004, 15:48:01

Job time : 60.5 secs

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Qy 121 TGACCCCTGCCCTGTGCC 138
Db 121 TGACCCCTGCCCTGTGCC 138

RESULT 5
US-10-017-273A-1
; Sequence 1, Application US/10017273A
; Publication No. US20030119714A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Naylor, Alasdair M.
; APPLICANT: Van Der Graaf, Pieter H
; APPLICANT: Wayman, Christopher P.
; TITLE OF INVENTION: Treatment of Male Sexual Dysfunction
; FILE REFERENCE: P222013
; CURRENT APPLICATION NUMBER: US/10/017,273A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/265,358
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: GB 0030647.2
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: GB 0108730.3
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: GB 0120679.6
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 09/905,846
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/291,722
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 09/895,367
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-017-273A-1

Query Match 100.0%; Score 138; DB 15; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60
Db 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60

Qy 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120

Qy 121 TGACCCCTGCCCTGTGCC 138
Db 121 TGACCCCTGCCCTGTGCC 138

RESULT 6
US-10-191-997-94
; Sequence 94, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: ARROW, Amy
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: NPY: Acc. No. US20030207834A1 K01911
US-10-191-997-94

Query Match 100.0%; Score 138; DB 16; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60
Db 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60

Qy 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120

Qy 121 TGACCCCTGCCCTGTGCC 138
Db 121 TGACCCCTGCCCTGTGCC 138

RESULT 7
US-10-036-542-16
; Sequence 16, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002p1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (118)..(118)
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; NAME/KEY: misc_feature
; LOCATION: (254)..(255)
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; OTHER INFORMATION: n equals a,t,g, or c  
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; LOCATION: (887)..(887)  
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; LOCATION: (897)..(897)  
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US-10-036-542-16

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Best Local Similarity 96.9%; Pred. No. 3.8e-31;  
Matches 126; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 9 CGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACCCAC 68  
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Db 250 CGAGNNCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACCCAC 309  
QY 69 GCCCGGGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGACTGACCCCTC 128  
|||  
Db 310 GCCCGGGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGACTGACCCCTC 369  
QY 129 GCCCTGTCCC 138  
|||  
Db 370 GCCCTGTCCC 379

RESULT 8  
US-10-036-542-41  
; Sequence 41, Application US/10036542  
; Publication No. US20030083481A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins  
; FILE REFERENCE: PA002P1  
; CURRENT APPLICATION NUMBER: US/10/036,542  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: PCT/US00/19666  
; PRIOR FILING DATE: 2000-07-20  
; PRIOR APPLICATION NUMBER: 60/144,972  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 60/148,681  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/149,173  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/158,004  
; PRIOR FILING DATE: 1999-10-06  
; PRIOR APPLICATION NUMBER: 60/194,689  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 157  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; TYPE: DNA  
; LENGTH: 553  
; ORGANISM: Homo sapiens  
US-10-036-542-41

Query Match 80.4%; Score 111; DB 15; Length 553;  
Best Local Similarity 99.2%; Pred. No. 1.2e-26;  
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 16 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACCCGCGG 75  
Db 1 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACCCGCGG 60  
QY 76 CGCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGACTGACCCCTGCTGT 135  
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Db 61 CGCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGACTGACCCCTGCTGT 119  
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QY 136 CCC 138  
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Db 120 CCC 122

RESULT 9  
US-09-925-300-100  
; Sequence 100, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 100  
; LENGTH: 599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (583)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (584)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (599)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-100

Query Match 80.4%; Score 111; DB 9; Length 599;  
Best Local Similarity 99.2%; Pred. No. 1.2e-26;  
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 16 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACCCGCGG 75  
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Db 14 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACCCGCGG 73  
QY 76 CGCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGACTGACCCCTGCTGT 135  
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Db 74 CGCCA-CCCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGACTGACCCCTGCTGT 132  
QY 136 CCC 138  
|||  
Db 133 CCC 135

RESULT 10  
US-10-036-542-42  
; Sequence 42, Application US/10036542  
; Publication No. US20030083481A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins  
; FILE REFERENCE: PA002P1  
; CURRENT APPLICATION NUMBER: US/10/036,542  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: PCT/US00/19666  
; PRIOR FILING DATE: 2000-07-20  
; PRIOR APPLICATION NUMBER: 60/144,972  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 60/148,681  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/149,173  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/158,004  
; PRIOR FILING DATE: 1999-10-06



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; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (583)..(584)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (599)..(599)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-036-542-42

Query Match      80.4%; Score 111; DB 15; Length 599;
Best Local Similarity 99.2%; Pred. No. 1.2e-26;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 16 TCTCACCCTCGGAGAGCTCGCCGACAGCATAGTACTGCCGCCGACGACGCGCCGCG 75
Db 14 TCTCACCCTCGGAGAGCTCGCCGACAGCATAGTACTTGCCGCCGACGACGCGCCGCG 73

QY 76 CGCCAGCCACCATCTAGGTAAACAAGGACTGGGGCTGTCCGGACTGACCTCGCCCTGT 135
Db 74 CGCCA-CCACCATCTAGGTAAACAAGGACTGGGGCTGTCCGGACTGACCTCGCCCTGT 132

QY 136 CCC 138
Db 133 CCC 135

RESULT 11
US-10-069-129-1
; Sequence 1, Application US/10069129
; Publication No. US20030224362A1
; GENERAL INFORMATION:
; APPLICANT: Jussi Kauhane, Matti Karvonen, Ullamari Pesonen, Markku Koulu, Matti
; APPLICANT: Uusitupa
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Alcoholism Based on Leucine7 to Proline 7 Polymorphism in the P
; TITLE OF INVENTION: Neuropeptide
; TITLE OF INVENTION: Y Gene, and methods for the prevention and Treatment of Alcoholi
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/069,129
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-069-129-1

Query Match      65.9%; Score 91; DB 13; Length 325;
Best Local Similarity 90.7%; Pred. No. 3.9e-20;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGCCGC 60
Db 210 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGCCGC 269

QY 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGTAAACAGCGACTG 107
Db 270 CCAGCCACGCGCGCGCCGACGACCATGCTAGTAAACAGCGACTG 316

RESULT 12
US-10-002-048A-3
; Sequence 3, Application US/10002048A
; Publication No. US20002018261A1
; GENERAL INFORMATION:
; APPLICANT: Wahlestedt, Claes
; APPLICANT: Ding, Bo
; TITLE OF INVENTION: Single Nucleotide Polymorphisms
; FILE REFERENCE: 10806-143
; CURRENT APPLICATION NUMBER: US/10/002,048A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: SE 0004035-2
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 325
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: prim_transcript
; LOCATION: (210)..(325)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank/M14295
; DATABASE ENTRY DATE: 1995-01-08
US-10-002-048A-3

Query Match      65.9%; Score 91; DB 14; Length 325;
Best Local Similarity 90.7%; Pred. No. 3.9e-20;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGCCGC 60
Db 210 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGCCGC 269

QY 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGTAAACAGCGACTG 107
Db 270 CCAGCCACGCGCGCGCCGACGACCATGCTAGTAAACAGCGACTG 316

RESULT 13
US-10-236-903-1
; Sequence 1, Application US/10236903
; Publication No. US20030093821A1
; GENERAL INFORMATION:
; APPLICANT: Hormos Medical Oy, Ltd.
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant Prepro-Neuropeptide Y, a Mutant
; TITLE OF INVENTION: Peptide, and Uses Thereof
; FILE REFERENCE: 2328-126
; CURRENT APPLICATION NUMBER: US/10/236,903
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/472,188
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 08/994,946
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-236-903-1

Query Match      65.9%; Score 91; DB 15; Length 325;
Best Local Similarity 90.7%; Pred. No. 3.9e-20;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGCCGC 60
Db 210 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGCCGC 269
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**Qy** 61 CCAGCCACGCCGCGCGCCAGCCACCATGTCTAGGTAAACAAGCGACTG 107  
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**pB** 270 CCAGCCACGCCGCGCGCCAGCCACCGTGA GTGTGCTACGACC CGTCTG 316  
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## RESULT 14

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US-10-027-632-127333/C
; Sequence 127333, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127333
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-127333

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## RESULT 15

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RESULTS 13
US/10-027-632-127333/c
; Sequence 127333, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of single Nucleotide
; polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; CURRENT APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 860 Seconds  
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Title: US-09-645-590-2

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_htg.*
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13: gb_un.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	136.4	98.8	551	6	ARI76719	ARI76719 Sequence
2	136.4	98.8	551	6	AXI38816	AXI38816 Sequence
3	136.4	98.8	551	6	AXI39001	AXI39001 Sequence
4	136.4	98.8	551	6	AXI39420	AXI39420 Sequence
5	136.4	98.8	551	6	AX337554	AX337554 Sequence
6	136.4	98.8	551	6	AX463054	AX463054 Sequence
7	136.4	98.8	551	6	BD015786	BD015786 Compound
8	136.4	98.8	551	6	BD015859	BD015859 Compound
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11	136.4	98.8	551	11	GI8330	GI8330 swSS1475 Er
12	136.4	98.8	568	9	BC029497	BC029497 Homo sapi
13	136.4	98.8	568	9	AR416737	AR416737 Sequence
14	111.6	80.9	122	6	BD112290	BD112290 EST and e
15	89.4	64.8	325	6	ARI76715	ARI76715 Sequence
16	89.4	64.8	325	6	BD103557	BD103557 Variant p
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18	89.4	64.8	185516	9	AC004485	AC004485 Homo sapi
19	88.6	64.2	182634	9	AC142353	AC142353 Pan trogl
20	88.6	64.2	230701	2	AC147298	AC147298 Pan trogl
21	84.2	61.0	169	6	AX897763	AX897763 Sequence
22	84.2	61.0	169	6	BD033296	BD033296 Sequence
23	68	49.3	561	10	BC043012	BC043012 Mus muscu
24	63.8	46.2	452	4	QAR417904	AJ417904 Ovis arie
25	61.6	44.6	511	10	RATNPYA	M20373 Rat neurope
26	61.6	44.6	539	10	RATNPY	M15860 Rat neurope
27	61.6	44.6	707	6	AX525587	AX525587 Sequence
28	61.4	44.5	483	6	AX305379	AX305379 Sequence
29	61.2	44.3	417	9	HUMNPYA	M15789 Human neuro
30	58.8	42.6	411	9	AF162280	AF162280 Magaca mu
31	50.4	36.5	247	6	ARI76716	ARI76716 Sequence
32	50.4	36.5	247	6	BD103558	BD103558 Variant p
33	50.4	36.5	247	9	HUMNPY02	BD103558 Variant p
34	49	35.5	130	6	AX897762	M14296 Human neuro
35	49	35.5	130	6	BD033295	AX897762 Sequence
36	41	29.7	1022	6	AX597893	BD033295 Sequence
37	40.8	29.6	269	10	AF286198	AX597893 Sequence
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41	40.8	29.6	8102	10	AF392060	M15792 Rat neurope
42	40.8	29.6	8103	10	AF392057	AF392060 Rattus no
43	40.8	29.6	8104	10	AF392059	AF392057 Rattus no
44	40.8	29.6	8105	10	AF392058	AF392059 Rattus no
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# ALIGNMENTS

RESULT 1  
ARI76719  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

ARI76719  
Sequence 5 from patent US 6312898.  
ARI76719  
ARI76719.1 GI:17919074  
Unknown.  
Unclassified.  
1 (bases 1 to 551)  
Koulu, M., Karvonen, M., Pesonen, U. and Uusitupa, M.  
Diagnosis of a person's risk of developing atherosclerosis or  
diabetic retinopathy based on leucine 7 to proline 7 polymorphism  
in the prepro-neuropeptide Y gene

linear PAT 17-DEC-2001

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JOURNAL Patent: US 6312898-A 5 06-NOV-2001;
FEATURES Location/Qualifiers
SOURCE 1..551
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 98.8%; Score 136.4; DB 6; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.3e-22;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60

QY 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120

QY 121 TGACCCCTGCGCCCTGTCCC 138
Db 121 TGACCCCTGCGCCCTGTCCC 138

RESULT 2
AX138816 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097706.
ACCESSION AX138816
VERSION AX138816.1 GI:14274563
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE Phosphodiesterase inhibitors for the treatment of female sexual
dysfunction
JOURNAL Patent: EP 1097706-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES Location/Qualifiers
SOURCE 1..551
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.8%; Score 136.4; DB 6; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.3e-22;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60

QY 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120

QY 121 TGACCCCTGCGCCCTGTCCC 138
Db 121 TGACCCCTGCGCCCTGTCCC 138

RESULT 3
AX139001 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097707.
ACCESSION AX139001
VERSION AX139001.1 GI:14274691
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE New inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES Location/Qualifiers
SOURCE 1..551
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
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Best Local Similarity 99.3%; Pred. No. 2.3e-22;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60

QY 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120

QY 121 TGACCCCTGCGCCCTGTCCC 138
Db 121 TGACCCCTGCGCCCTGTCCC 138

RESULT 4
AX139420 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097719.
ACCESSION AX139420
VERSION AX139420.1 GI:14275073
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE New inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES Location/Qualifiers
SOURCE 1..551
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.8%; Score 136.4; DB 6; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.3e-22;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60
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QY 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120
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QY 121 TGACCCCTGCGCCCTGTCCC 138
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RESULT 5
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LOCUS
DEFINITION Sequence 8 from Patent EP1097719.
ACCESSION AX139420
VERSION AX139420.1 GI:14275073
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE New inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 98.8%; Score 136.4; DB 6; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.3e-22;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCCG 60

QY 61 CCAGCCACGCCCGCGCGGCGGACGACCATGCTAGGTAAACAGGACCGGGGCTGTCCGGAC 120
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QY 121 TGACCCCTGCGCCCTGTCCC 138
Db 121 TGACCCCTGCGCCCTGTCCC 138
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RESULT 8
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LOCUS       BD015859             551 bp    DNA        linear    PAT 27-AUG-2002
DEFINITION  Compound for treatment of female sexual dysfunction.
ACCESSION   BD015859
VERSION     BD015859.1  GI:22556996
KEYWORDS    JP 2001213802-A/4.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
AUTHORS     Maw G.N. and Wayman C.P.
TITLE       Compound for treatment of female sexual dysfunction
JOURNAL     Patent: JP 2001213802-A 4 07-AUG-2001;
            PFIZER INC
COMMENT     OS Homo sapiens (human)
            PN JP 2001213802-A/4
            PD 07-AUG-2001
            PR 08-NOV-2000 JP 2000339853
            PR 08-NOV-1999 JP 9926437.6,18-FEB-2000 GB 0004021.2 PR
            PR 26-MAY-2000 GB 0013001.3,05-JUL-2000 GB 0016563.9 PR
            PR 12-JUL-2000 GB 0017141.3
            PI GRAHAM NIGEL MAW,CHRISTOPHER PETER WAYMAN
            PC A61K45/00,A61K31/19,A61K31/192,A61K31/4015,A61K31/433,A61K31/
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            CC Compound for treatment of female sexual dysfunction PH Key
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Query Match      98.8%; Score 136.4; DB 6; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.3e-22;
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QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCG 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCG 60
QY 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCGGGGCTGTCGGGAC 120
Db 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGAC 120
QY 121 TGACCTCGCCCTGTGCC 138
Db 121 TGACCTCGCCCTGTGCC 138

RESULT 9
BD103561
LOCUS       BD103561             551 bp    RNA        linear    PRI 07-JAN-1995
DEFINITION  Human neuropeptide Y (NPY) mRNA, complete cds.
ACCESSION   K01911
VERSION     K01911.1  GI:189273
KEYWORDS    neuropeptide Y.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
AUTHORS     Minth,C.D., Bloom,S.R., Polak,J.M. and Dixon,J.E.
TITLE       Cloning, characterization, and DNA sequence of a human cDNA
            encoding neuropeptide tyrosine
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 81 (14), 4577-4581 (1984)
MEDLINE     84272678
PUBMED      6589611
COMMENT     Original source text: Human pheochromocytoma, cDNA to mRNA, clone
            pNPY3-75.
            Neuropeptide Y (NPY) is one of the most abundant peptides in the
            mammalian nervous system, and its extensive distribution suggests a
            neuro-transmitter or -modulator role. NPY is also found in some
            chromaffin cells of the adrenal medulla.

FEATURES             Location/Qualifiers
            1  (bases 1 to 551)

```

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AUTHORS       Koulu,M., Karvonen,M., Pesonen,U. and Uusitupa,M.
TITLE         Variant prepro-neuropeptide Y, DNA molecule encoding variant signal
            peptide and utilization of the same
JOURNAL       Patent: JP 2001526296-A 5 18-DEC-2001;
            HORMOS MEDICAL OY LTD
COMMENT       OS Unidentified
            PN JP 2001526296-A/5
            PD 18-DEC-2001
            PR 16-DEC-1998 JP 2000525455
            PR 19-DEC-1997 US 08/994946
            PI MARKKU KOULU,MATTI KARVONEN ULLAMARI PESONEN MATTI UUSITUPA PC
            C07K14/575,A01K67/027,A61K38/00,A61K38/22,A61K48/00,A61P3/06, PC
            A61P43/00,
            PC C07K16/26,C12N5/10,C12N15/09,C12Q1/68,G01N33/15,G01N33/50// PC
            C12P21/08,
            PC A61K37/02,A61K37/24,C12N5/00,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Variant prepro-neuropeptide Y, DNA molecule encoding variant
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            CC and utilization of the same
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Query Match      98.8%; Score 136.4; DB 6; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.3e-22;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCG 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCG 60
QY 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCGGGGCTGTCGGGAC 120
Db 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCGGGAC 120
QY 121 TGACCTCGCCCTGTGCC 138
Db 121 TGACCTCGCCCTGTGCC 138

RESULT 10
HUNNPY
LOCUS       HUNNPY             551 bp    mRNA        linear    PRI 07-JAN-1995
DEFINITION  Human neuropeptide Y (NPY) mRNA, complete cds.
ACCESSION   K01911
VERSION     K01911.1  GI:189273
KEYWORDS    neuropeptide Y.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
AUTHORS     Minth,C.D., Bloom,S.R., Polak,J.M. and Dixon,J.E.
TITLE       Cloning, characterization, and DNA sequence of a human cDNA
            encoding neuropeptide tyrosine
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 81 (14), 4577-4581 (1984)
MEDLINE     84272678
PUBMED      6589611
COMMENT     Original source text: Human pheochromocytoma, cDNA to mRNA, clone
            pNPY3-75.
            Neuropeptide Y (NPY) is one of the most abundant peptides in the
            mammalian nervous system, and its extensive distribution suggests a
            neuro-transmitter or -modulator role. NPY is also found in some
            chromaffin cells of the adrenal medulla.

FEATURES             Location/Qualifiers
            1  (bases 1 to 551)

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171. .278
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Best Local Similarity 99.3%; Pred. No. 2.3e-22;
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Qy 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCCG 60
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Qy 61 CCAGCCAGCCGCGCGCCGACGACCATGCTAGTAAACAGCGACCGGGCTGTCCGAC 120
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Qy 121 TGACCTCGCCCTGTCCC 138
Db 121 TGACCTCGCCCTGTCCC 138

RESULT 11
G18330
LOCUS
DEFINITION SW51475 Eric D. Green Homo sapiens STS genomic, sequence tagged
site
G18330
VERSION G18330.1 GI:1222787
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 551)
Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,
Leckie,M.P. and Green,E.D.
Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
97189344
MEDLINE
PUBMED 9037602
REFERENCE 2 (bases 1 to 551)
Green,E.D.
AUTHORS Human chromosome 7 STSs (1997)
TITLE Unpublished (1997)
JOURNAL
SYNOPSIS: NPY
GDB: GDB:3754247
GDB_DSEG: NPY

```

Contact: Eric D. Green  
Genome Technology Branch  
National Human Genome Research Institute/NIH  
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892  
Tel: 3014020201  
Fax: 3014024735  
Email: egreen@nhgri.nih.gov  
Primer A: CCACCATCTTACCAATG  
Primer B: GACAAAGGAAAACATTGCAG  
STS size: 60  
PCR Profile:

Presoak: 0 degrees C for 0.00 minute(s)  
Denaturation: 92 degrees C for 0.17 minute(s)  
Annealing: 55 degrees C for 1.00 minute(s)  
Polymerization: 72 degrees C for 1.00 minute(s)  
PCR Cycles: 35  
Thermal Cycler: PerkinElmer 9600  
Protocol:

Template: 30-100 ng  
each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 8.3

This STS was developed from sequence determined by another investigator. See GenBank record: K01911 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/STB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID=92128937].

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Query Match 98.8%; Score 136.4; DB 11; Length 551;  
Best Local Similarity 99.3%; Pred. No. 2.3e-22;  
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCCG 60  
Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCCG 60  
Qy 61 CCAGCCAGCCGCGCGCCGACGACCATGCTAGTAAACAGCGACCGGGCTGTCCGAC 120  
Db 61 CCAGCCAGCCGCGCGCGCCGACGACCATGCTAGTAAACAGCGACCGGGCTGTCCGAC 120  
Qy 121 TGACCTCGCCCTGTCCC 138  
Db 121 TGACCTCGCCCTGTCCC 138

RESULT 12  
BC029497  
LOCUS  
DEFINITION BC029497 568 bp mRNA linear PRI 06-OCT-2003  
Homo sapiens neuropeptide Y, mRNA (cDNA clone MGC:33138  
IMAGE:5278692), complete cds.

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ACCESSION      BC029497
VERSION        BC029497.1  GI:20809582
KEYWORDS       MGC.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 568)
AUTHORS        Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
               Klatsner,R.D., Collins,F.S., Wagner,L., Shenker,C.M., Schuler,G.D.,
               Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
               Hopkins,R.F., Jordan,H., Moore,T.J., Max,S.I., Wang,J., Hsieh,F.,
               Diatchenko,L., Marusich,K., Farmer,A.A., Rubin,G.M., Hong,L.,
               Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
               Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
               Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
               Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
               McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
               Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
               Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
               Fahey,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
               Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
               Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
               Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
               Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
               Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
               Generation and initial analysis of more than 15,000 full-length
               human and mouse cDNA sequences
               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
               22388257
               12477932
               2 (bases 1 to 568)
               Strausberg,R.
               Direct Submission
               Submitted (01-MAY-2002) National Institutes of Health, Mammalian
               Gene Collection (MGC), Cancer Genomics Office, National Cancer
               Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
               USA
               NIH-MGC Project URL: http://mgc.nci.nih.gov
               Contact: MGC help desk
               Email: cgabs-r@mail.nih.gov
               Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
               cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
               Toshiyuki and Piero Carninci (RIKEN)
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
               DNA Sequencing by: Sequencing Group at the Stanford Human Genome
               Center, Stanford University School of Medicine, Stanford, CA 94305
               Web site: http://www-shgc.stanford.edu
               Contact: (Dickson, Mark) mcd@paxil.stanford.edu
               Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
               R. M.
               Clone distribution: MGC clone distribution information can be found
               through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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               Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
               QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACAGCATAGTAGTTCGCCGC 60
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               Db 63 CCAGCCAGCCGCCGCCGAGCAGCAGCATAGTCTAGGTAAACAAGGACCTGTCCGGAC 122
               QY 121 TCACCTCGCCCTGTCCC 138
               Db 123 TCACCTCGCCCTGTCCC 140
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               AR416737
               VERSION
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               Unclassified.
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               1 (bases 1 to 122)
               AUTHORS
               Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
               TITLE
               EST's and encoded human proteins
               JOURNAL
               Patent: US 6639063-A 8234 28-OCT-2003;
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               Db 121 TG 122
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               LOCUS
               DEFINITION
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               ACCESSION
               BD112290
               VERSION
               BD112290.1 GI:23207108
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               JP 2002010789-A/4367.
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               Homo sapiens (human)

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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS       1 (bases 1 to 122)
TITLE         Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
JOURNAL       Patent: JP 2002010789-A 4367 15-JAN-2002;
               GENSET CORP
COMMENT       OS Homo sapiens (human)
               PN JP 2002010789-A/4367
               PD 15-JAN-2002
               PF 07-AUG-2000 JP 2000280989
               PR 05-AUG-1999 US 60/147499
               PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
               GIORDANO
               PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
               C12N1/21,
               PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
               C12N15/00
               CC EST and encoded human protein
               FH Key
               FT source
               FT source
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               1..122
               /organism="Homo sapiens (human)"
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Query Match      80.9%; Score 111.6; DB 6; Length 122;
Best Local Similarity 93.4%; Pred. No. 2.1e-16;
Matches 114; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGC CGC 60
Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGC CGC 60

QY 61 CCAGCCAGCCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCG 120
Db 1 CCAGCCAGCCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCG 120

QY 121 TG 122
Db 121 TG 122

RESULT 15
AR176715
LOCUS          325 bp DNA linear PAT 17-DEC-2001
DEFINITION     Sequence 1 from patent US 6312898.
ACCESSION      AR176715
VERSION        AR176715.1 GI:17919070
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 325)
AUTHORS        Koulu, M., Karvonen, M., Pesonen, U. and Uusitupa, M.
TITLE         Diagnosis of a person's risk of developing atherosclerosis or
               diabetic retinopathy based on leucine 7 to proline 7 polymorphism
               in the prepro-neuropeptide Y gene
JOURNAL        Patent: US 6312898-A 1 06-NOV-2001;
FEATURES       Location/Qualifiers
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               /mol_type="unassigned DNA"

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Best Local Similarity 89.7%; Pred. No. 3.1e-11;
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGC CGC 60
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QY 61 CCAGCCAGCCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCG 107
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Job time : 861 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 272 Seconds  
(without alignments)  
2155.336 Million cell updates/sec

Title: US-09-645-590-2

Perfect score: 138

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	136.4	98.8	138	6	AAL42206 Human neu
2	136.4	98.8	138	6	AAL42205 Human neu
3	136.4	98.8	551	2	AAX86051 cDNA enco
4	136.4	98.8	551	3	AAC60348 Human neu
5	136.4	98.8	551	4	AAD14527 Human neu
6	136.4	98.8	551	4	AAD14517 Human neu
7	136.4	98.8	551	4	AAF84086 Human neu
8	136.4	98.8	551	4	AAF84076 Human neu
9	136.4	98.8	551	6	ABL69726 Prostate
10	136.4	98.8	551	6	ABN84276 Human neu
11	136.4	98.8	551	6	AAL47339 Human neu
12	136.4	98.8	551	7	ACF63372 Human neu
13	123.2	89.3	969	4	AAF72746 Human pro
14	109.4	79.3	553	4	AAF72771 Human pro
15	109.4	79.3	599	3	AAF15665 Human pro
16	109.4	79.3	599	4	AAF72772 Human pro
17	89.4	64.8	325	2	AAX86047 Exon 1 of
18	89.4	64.8	325	3	AAC60344 Human neu
19	89.4	64.8	325	6	AAL47340 Human neu
20	89.4	64.8	722	6	AAL47344 Human neu
21	89.4	64.8	14537	6	AAL48078 Human neu
22	89.2	64.6	609	5	ABV35249 Human pro
23	89.2	64.6	609	5	ABV44088 Human pro

24	87.8	63.6	496	8	ACH15527 Human adu
25	87.6	63.5	696	5	ABV04986 Human pro
26	87.4	63.3	683	5	ABV14155 Human pro
27	85.4	61.9	562	5	ABV23158 Human pro
28	85.4	61.9	562	5	ABV28999 Human pro
29	84.2	61.0	169	3	AAC09551 Human sec
30	61.6	44.6	539	9	ADB52549 Primary r
31	61.6	44.6	707	6	ABT09021 Phase-1 r
32	61.4	44.5	483	6	AB199285 Mouse isc
33	61.4	44.5	1185	5	ABV29161 Human pro
34	61.4	44.5	1185	5	ABV21898 Human pro
35	61.4	44.5	1185	5	ABV27730 Human pro
36	61.4	44.5	1185	5	ABV24480 Human pro
37	61.4	44.5	1185	5	ABV22222 Human pro
38	61.4	44.5	1185	5	ABV22776 Human pro
39	61.4	44.5	1185	5	ABV21541 Human pro
40	61.4	44.5	1185	5	ABV27360 Human pro
41	61.4	44.5	1185	5	ABV28602 Human pro
42	61.4	44.5	1185	5	ABV23315 Human pro
43	61.4	44.5	1185	5	ABV28059 Human pro
44	61.2	44.3	417	9	ADB75464 Prostate
45	50.4	36.5	247	2	AAX86048 Exon 2 of

## ALIGNMENTS

RESULT 1  
AAL42206  
ID AAL42206 standard; mRNA; 138 BP.  
XX  
AC AAL42206;  
XX  
DT 13-JUN-2002 (first entry)  
XX  
DE Human neurotensin Y (NPY) mRNA sequence, binding structure 2.  
XX  
KW Human; ss; stress-induced neurotensin Y overproduction; NPY;  
KW neurotransmitter; central nervous system; peripheral nervous system;  
KW heart rate reduction; insulin secretion enhancement; NPY mRNA;  
KW binding structure 2.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT stem\_loop 10..38 /\*tag= a  
FT misc\_binding 41..46 /\*tag= b  
FT /\*bound moiety= "Human neurotensin Y (NPY) mRNA"  
FT /\*note= "Forms a double stranded region with bases 115-110 of itself"  
FT stem\_loop 50..68 /\*tag= c  
FT stem\_loop 70..109 /\*tag= d  
FT misc\_binding 110..115 /\*tag= e  
FT /\*bound moiety= "Human neurotensin Y (NPY) mRNA"  
FT /\*note= "Forms a double stranded region with bases 46-41 of itself"  
FT stem\_loop 117..137 /\*tag= f  
WO200215941-A1.  
28-FEB-2002.  
XX  
31-JUL-2001; 2001WO-FI000687.  
XX  
25-AUG-2000; 2000US-00645590.  
XX  
PA (HORM-) HORMOS MEDICAL CORP.



XX (HORM-) HORMOS MEDICAL LTD OY.  
 PA Koulu M, Karvonen M, Pesonen U, Uusitupa M;  
 PI WPI; 1999-405161/34.  
 XX P-PSDB; AAY23828.  
 DR New polynucleotide (I) encoding a prepro-neuropeptide Y (preproNPY).  
 XX Claim 2; Fig 1c; 45pp; English.  
 PT The present sequence encodes human prepro-neuropeptide Y (NPY). The  
 CC specification describes a polynucleotide encoding a prepro-neuropeptide Y  
 CC (preproNPY), where leu (7) is substituted by pro(7). This polynucleotide  
 CC is useful for diagnosing and treating humans with a predisposition for  
 CC increased serum cholesterol or low density lipoprotein (LDL)  
 XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 SQ

Query Match 98.8%; Score 136.4; DB 2; Length 551;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60  
 DB 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60  
 QY 61 CCAGCCAGCGCCGCGCGCCGACCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120  
 DB 61 CCAGCCAGCGCCGCGCGCCGACCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120  
 QY 121 TGACCCCTGCCCTGTGCC 138  
 DB 121 TGACCCCTGCCCTGTGCC 138

RESULT 4  
 AAC60348  
 ID AAC60348 standard; DNA; 551 BP.  
 AC AAC60348;  
 XX 16-FEB-2001 (first entry)  
 DT Human neuropeptide Y coding DNA.  
 DE NPY; neuropeptide Y; gene therapy; atherosclerosis; diabetic retinopathy;  
 KW ds.  
 XX Homo sapiens.  
 OS WO200063430-A1.  
 XX 26-OCT-2000.  
 XX 29-MAR-2000; 2000WO-FI000260.  
 XX 15-APR-1999; 99US-00291994.  
 XX (HORM-) HORMOS MEDICAL LTD OY.  
 XX Koulu M, Karvonen M, Pesonen U, Uusitupa M;  
 XX WPI; 2000-679606/66.  
 DR Diagnosing diabetic person's susceptibility for developing  
 PT atherosclerosis or diabetic retinopathy involves detecting leucine7 to  
 PT proline7 polymorphism in signal peptide part of human prepro neuropeptide  
 XX Y.  
 XX Disclosure; Fig 1; 4lpp; English.

CC The present invention relates to diagnosing a diabetic person's  
 CC susceptibility for having an increased risk of developing atherosclerosis  
 CC or diabetic retinopathy involves determining whether the subject has a  
 CC substitution of leucine 7 for proline in the signal peptide part of human  
 CC prepro-neuropeptide Y  
 XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 SQ

Query Match 98.8%; Score 136.4; DB 3; Length 551;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60  
 DB 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60  
 QY 61 CCAGCCAGCGCCGCGCGCCGACCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120  
 DB 61 CCAGCCAGCGCCGCGCGCCGACCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120  
 QY 121 TGACCCCTGCCCTGTGCC 138  
 DB 121 TGACCCCTGCCCTGTGCC 138

RESULT 5  
 AAD14527  
 ID AAD14527 standard; DNA; 551 BP.  
 AC AAD14527;  
 XX 01-NOV-2001 (first entry)  
 DT Human neuropeptide Y (NPY) DNA.  
 DE Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;  
 KW FSAD; neutral endopeptidase inhibitor; I:NEP; enkephalinase;  
 XX gynaecological; endopeptidase-2; neuropeptide Y; NPY; ds.  
 OS Homo sapiens.  
 PH Key Location/Qualifiers  
 FT CDS 87..380  
 FT /\*tag= a  
 FT /product= "Human NPY"  
 FT sig\_peptide 87..170  
 FT /\*tag= b  
 FT mat\_peptide 171..278  
 FT /\*tag= c  
 FT /product= "Human mature NPY protein"  
 XX EPI097719-A1.  
 XX 09-MAY-2001.  
 XX 03-NOV-2000; 2000EP-00309722.  
 XX 08-NOV-1999; 99GB-00026437.  
 XX 18-FEB-2000; 2000GB-00004021.  
 XX 26-MAY-2000; 2000GB-00013001.  
 XX 05-JUL-2000; 2000GB-00016563.  
 XX 12-JUL-2000; 2000GB-00017141.  
 XX (PFIZ ) PFIZER LTD.  
 XX (PFIZ ) PFIZER INC.  
 XX Maw GN, Wayman CP;  
 XX WPI; 2001-309880/33.  
 XX P-PSDB; AAE07955.  
 XX Treating females suffering from female sexual dysfunction, preferably  
 PT female sexual arousal dysfunction using a neutral endopeptidase inhibitor

PT that potentiates cAMP in female genitalia.  
 PS Disclosure; Page 97; 124pp; English.  
 XX  
 CC The present invention relates to a method for treating female sexual  
 CC dysfunction (FSD), preferably female sexual arousal dysfunction (FSAD).  
 CC The method comprising using an agent, an inhibitor of neutral  
 CC endopeptidase (NEP) EC 3.4.24.11 or I-NEP, which is capable of  
 CC potentiating cAMP (which enhances female genital blood flow) in the  
 CC sexual genitalia of the females. NEP is also known as enkephalinase or  
 CC endopeptidase-2. The agent is optionally admixed with a diluent, carrier  
 CC or excipient. The method restores a normal sexual arousal response,  
 CC particularly increased blood flow leading to vaginal, clitoral and labial  
 CC engorgement. This will result in increased vaginal lubrication via plasma  
 CC transduction, increased vaginal compliance and increased genital (e.g.  
 CC vaginal and clitoral) sensitivity. The present sequence is human  
 CC neuropeptide Y (NPY) DNA used in the method of the invention  
 XX  
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 Query Match 98.8%; Score 136.4; DB 4; Length 551;  
 Best Local Similarity 99.3%; Pred. NO. 2.7e-29;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGC 60  
 Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGC 60  
 QY 61 CCAGCCACGCCGCGCGCCGAGCCACCATCTAGGTAAACGAGCCGCGGCTGTCCGGAC 120  
 Db 61 CCAGCCACGCCGCGCGCCGAGCCACCATCTAGGTAAACGAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCTCGCTGTGCC 138  
 Db 121 TGACCTCGCTGTGCC 138  
 RESULT 6  
 AAD14517 standard; DNA; 551 BP.  
 AC AAD14517;  
 XX 01-NOV-2001 (first entry)  
 XX Human neuropeptide Y (NPY) DNA.  
 DE Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;  
 KW FSAD; neuropeptide Y; NPY; gynaecological; vasoactive intestinal peptide;  
 KW VIP; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 87..380  
 FT /\*tag= a  
 FT /product= "Human NPY protein"  
 FT sig\_peptide 87..170  
 FT /\*tag= b  
 FT mat\_peptide 171..278  
 FT /\*tag= c  
 FT /product= "Human mature NPY protein"  
 XX  
 DN EP1097718-A1.  
 XX  
 XX 09-MAY-2001.  
 XX  
 XX 03-NOV-2000; 2000EP-00309720.  
 XX  
 XX 08-NOV-1999; 99GB-00026437.  
 PR 18-FEB-2000; 2000GB-00004021.  
 PR 26-MAY-2000; 2000GB-00013001.  
 PR 05-JUL-2000; 2000GB-00016563.  
 PR

PR 12-JUL-2000; 2000GB-00017141.  
 XX (PRIZ ) PFIZER LTD.  
 PA (PFIZ ) PFIZER INC.  
 XX  
 XX Maw GN, Wayman CP;  
 PI WPI: 2001-319199/34.  
 DR P-PSDB; AAE07919.  
 XX  
 XX Treating females suffering from female sexual dysfunction, preferably  
 XX female sexual arousal dysfunction using a neuropeptide Y inhibitor that  
 XX potentiates cAMP in female genitalia.  
 XX  
 XX Disclosure; Page 129; 165pp; English.  
 XX  
 XX The patent discloses a method for the treatment of a female suffering  
 XX from female sexual dysfunction (FSD), preferably female sexual arousal  
 XX dysfunction (FSAD) by the use of an agent which is an inhibitor of  
 XX neuropeptide Y (NPY). The agent is capable of potentiating cAMP which  
 XX enhances female genital (e.g. vaginal or clitoral) blood flow in the  
 XX sexual genitalia of the female and is optionally admixed with a diluent  
 XX carrier or excipient. The method restores a normal sexual arousal  
 XX response namely, increased blood flow leading to vaginal, clitoral and  
 XX labial engorgement. This will result in increased vaginal lubrication via  
 XX plasma transduction, increased vaginal compliance and increased genital  
 XX (e.g. vaginal and clitoral) sensitivity. The method is used for treating  
 XX a female suffering from FSD preferably FSAD. The present sequence is a  
 XX DNA encoding human neuropeptide Y (NPY) protein. NPY exerts an inhibitory  
 XX influence over VIP-mediated vasorelaxation and NPY Y1 receptor  
 XX antagonists will facilitate the vasorelaxant effect of endogenous  
 XX vasoactive intestinal peptide (VIP) released during arousal and enhances  
 XX vaginal engorgement  
 XX  
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 Query Match 98.8%; Score 136.4; DB 4; Length 551;  
 Best Local Similarity 99.3%; Pred. NO. 2.7e-29;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGC 60  
 Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGC 60  
 QY 61 CCAGCCACGCCGCGCGCCGAGCCACCATCTAGGTAAACGAGCCGCGGCTGTCCGGAC 120  
 Db 61 CCAGCCACGCCGCGCGCCGAGCCACCATCTAGGTAAACGAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCTCGCTGTGCC 138  
 Db 121 TGACCTCGCTGTGCC 138  
 RESULT 7  
 AAF84086  
 ID AAF84086 standard; DNA; 551 BP.  
 XX  
 XX AAF84086;  
 XX  
 XX 22-AUG-2001 (first entry)  
 XX Human neuropeptide Y (NPY) encoding DNA.  
 DE Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;  
 KW genital; vaginal; clitoral; blood flow; cAMP; phosphodiesterase; PDE;  
 KW CGMP; medicament; human; neuropeptide Y; NPY; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 87..380  
 FT /\*tag= a  
 FT /product= "neuropeptide Y"

FT	sig_peptide	/gene= "NPY"
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FT	mat_peptide	171..377
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XX	EP1097707-A1.	
XX		
XX	09-MAY-2001.	
XX		
XX	03-NOV-2000; 2000EP-00309719.	
PR	08-NOV-1999; 99GB-00026437.	
PR	18-FEB-2000; 2000GB-00004021.	
PR	26-MAY-2000; 2000GB-00013001.	
PR	05-JUL-2000; 2000GB-00016563.	
PR	12-JUL-2000; 2000GB-00017141.	
XX		
PA	(PFIZ ) PFIZER LTD.	
PA	(PFIZ ) PFIZER INC.	
XX		
XX	Maw GN, Wayman CP;	
XX		
DR	WPI; 2001-383217/41.	
DR	P-PSDB; AAB85118.	
XX		
XX	Novel pharmaceutical composition for treating female sexual dysfunction, preferably female sexual arousal disorder, comprising an agent capable of potentiating cAMP in the sexual genitalia of the female.	
XX	Disclosure; Page 104; 135pp; English.	
XX		
CC	The invention provides a pharmaceutical composition for treating female sexual dysfunction (FSD), preferably female sexual arousal disorder (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow in a female. The composition comprises an agent capable of potentiating cAMP in the sexual genitalia of the female. The agent is an inhibitor (I:PDR) of phosphodiesterase (PDE), which hydrolyzes cAMP (optionally cGMP). The agent is useful in the manufacture of a medicament for the treatment of FSD, preferably FSAD, by potentiating cAMP in the sexual genitalia. It is also useful in the manufacture of a medicament for enhancing female genital (e.g., vaginal or clitoral) blood flow. The present sequence represents a human neuropeptide Y (NPY) encoding DNA	
XX		
XX	Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;	
	Query Match	98.8%; Score 136.4; DB 4; Length 551;
	Best Local Similarity	99.3%; Pred. No. 2.7e-29;
	Matches 137; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1	ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCG 60
Db	1	ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCG 60
QY	61	CCAGCCACGCCCGCGCGCCACCATGCTAGGTAAACAGCAGCCGGGCTGTCCGAC 120
Db	61	CCAGCCACGCCCGCGCGCCACCATGCTAGGTAAACAGCAGCTGGGCTGTCCGAC 120
QY	121	TGACCCCTCGCCCTGTCCC 138
Db	121	TGACCCCTCGCCCTGTCCC 138
RESULT 8		
AAF84076		
ID	AAF84076 standard; DNA; 551 BP.	
XX		
XX	AAF84076;	
XX		
XX	22-AUG-2001 (first entry)	
DT		
XX	Human neuropeptide Y (NPY) encoding DNA.	
XX		

KW	Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
KW	genital; vaginal; clitoral; blood flow; CAMP; phosphodiesterase; PDE;
KW	cGMP; medicament; human; neuropeptide Y; NPY; ds.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	87..380
CDS	/tag= a
FT	/product= "neuropeptide y"
FT	/gene= "NPY"
FT	87..170
sig_peptide	/tag= b
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PN	EP1097706-A1.
XX	
PD	09-MAY-2001.
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PF	03-NOV-2000; 2000EP-00309718.
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PR	08-NOV-1999; 99GB-00026437.
PR	18-FEB-2000; 2000GB-00004021.
PR	26-MAY-2000; 2000GB-00013001.
PR	05-JUL-2000; 2000GB-00016563.
PR	12-JUL-2000; 2000GB-00017141.
XX	
PA	(PFIZ ) PFIZER LTD.
PA	(PFIZ ) PFIZER INC.
XX	
PI	Maw GN, Wayman CP;
XX	
DR	WPI; 2001-383216/41.
DR	P-FSDB; AAB85107.
XX	
PT	Novel pharmaceutical composition for treating female sexual dysfunction,
PT	preferably female sexual arousal disorder, comprising an agent capable of
PT	potentiating CAMP in the sexual genitalia of the female.
XX	
PS	Disclosure; Page 102; 132pp; English.
XX	
CC	The invention provides a pharmaceutical composition for treating female
CC	sexual dysfunction (FSD), preferably female sexual arousal disorder
CC	(FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow
CC	in a female. The composition comprises an agent capable of potentiating
CC	CAMP in the sexual genitalia of the female. The agent is an inhibitor
CC	(I-PDE) of phosphodiesterase (PDE), which hydrolyzes cAMP (optionally
CC	cGMP). The agent is useful in the manufacture of a medicament for the
CC	treatment of FSD, preferably FSAD, by potentiating CAMP in the sexual
CC	genitalia. It is also useful in the manufacture of a medicament for
CC	enhancing female genital (e.g., vaginal or clitoral) blood flow. The
CC	present sequence represents a human neuropeptide Y (NPY) encoding DNA
XX	
SQ	Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
Query Match	98.8%; Score 136.4; DB 4; Length 551;
Best Local Similarity	99.3%; Pred. No. 2.7e-29;
Matches 137; Conservative	0; Mismatches 1; Indels 0; Gaps 0
Qy	1 ACCCATTCGGTGGCTCTCACCCCTCGAGACGCTCGCCCCCAGCATAGTACTTGC CGC 60
Dd	
Db	1 ACCCATTCGGTGGCTCTCACCCCTCGAGACGCTCGCCCCCAGCATAGTACTTGC CGC 60
Qy	61 CCAGCCACGCCCGCGCCGACCACCATGCTAGGTAAACAAGCAGCGGGGTGTCCGGAC 120
Dd	
Db	61 CCAGCCACGCCCGCGCCGACCACCATGCTAGGTAAACAAGCAGCTGGGGGTGTCCGGAC 120
Qy	121 TGACCCCTGCGCCCTGTGCC 138
Dd	
Db	121 TGACCCCTGCGCCCTGTGCC 138

RESULT 9  
 ABL69726  
 ID ABL69726 standard; DNA; 551 BP.  
 XX AC ABL69726;  
 XX DT 15-MAY-2002 (first entry)  
 XX DE Prostate cancer related gene sequence SEQ ID NO:8063.  
 XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
 KW gene; ds.  
 XX OS Homo sapiens.  
 XX PN WO200194629-A2.  
 XX PD 13-DEC-2001.  
 XX PF 30-MAY-2001; 2001WO-US010838.  
 XX PR 05-JUN-2000; 2000US-0209473P.  
 PR 05-JUN-2000; 2000US-0209531P.  
 PR 18-SEP-2000; 2000US-0233133P.  
 PR 18-SEP-2000; 2000US-023317P.  
 PR 20-SEP-2000; 2000US-0234009P.  
 PR 20-SEP-2000; 2000US-0234034P.  
 PR 20-SEP-2000; 2000US-0234052P.  
 PR 22-SEP-2000; 2000US-0234509P.  
 PR 22-SEP-2000; 2000US-0234567P.  
 PR 25-SEP-2000; 2000US-0234923P.  
 PR 25-SEP-2000; 2000US-0234924P.  
 PR 25-SEP-2000; 2000US-0235077P.  
 PR 25-SEP-2000; 2000US-0235082P.  
 PR 25-SEP-2000; 2000US-0235134P.  
 PR 25-SEP-2000; 2000US-0235280P.  
 PR 26-SEP-2000; 2000US-0235637P.  
 PR 26-SEP-2000; 2000US-0235638P.  
 PR 27-SEP-2000; 2000US-0235711P.  
 PR 27-SEP-2000; 2000US-0235720P.  
 PR 27-SEP-2000; 2000US-0235843P.  
 PR 27-SEP-2000; 2000US-0235863P.  
 PR 28-SEP-2000; 2000US-0236028P.  
 PR 28-SEP-2000; 2000US-0236032P.  
 PR 28-SEP-2000; 2000US-0236033P.  
 PR 28-SEP-2000; 2000US-0236034P.  
 PR 28-SEP-2000; 2000US-0236109P.  
 PR 28-SEP-2000; 2000US-0236111P.  
 PR 29-SEP-2000; 2000US-0236842P.  
 PR 29-SEP-2000; 2000US-0236891P.  
 PR 02-OCT-2000; 2000US-0237172P.  
 PR 02-OCT-2000; 2000US-0237173P.  
 PR 02-OCT-2000; 2000US-0237278P.  
 PR 02-OCT-2000; 2000US-0237294P.  
 PR 02-OCT-2000; 2000US-0237295P.  
 PR 02-OCT-2000; 2000US-0237316P.  
 PR 03-OCT-2000; 2000US-0237425P.  
 PR 03-OCT-2000; 2000US-0237598P.  
 PR 03-OCT-2000; 2000US-0237604P.  
 PR 03-OCT-2000; 2000US-0237606P.  
 PR 03-OCT-2000; 2000US-0237608P.  
 PR 01-NOV-2000; 2000US-0244867P.  
 PR 01-NOV-2000; 2000US-0245084P.  
 XX (AVAL-) AVALON PHARM.  
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 XX WPI; 2002-188264/24.  
 DR XX

PT Screening for anti-neoplastic agent involves exposing cells to a chemical  
 PT agent to be tested for anti-neoplastic activity, and determining a change  
 XX in expression of a gene of a signature gene set.  
 XX Claim 1; SEQ ID NO 8063; 44pp; English.  
 XX The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
 CC to ABL70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC the data collected with respect to the anti-neoplastic agent as a result  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's  
 CC tumour  
 XX

SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;  
 Query Match 98.8%; Score 136.4; DB 6; Length 551;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ACCCCATCGCTGGTCTCACCCCTCGGAGAGCGTCTGCCGACAGCATAGTACTTGCCTGC 60  
 Db 1 ACCCCATCGCTGGTCTCACCCCTCGGAGAGCGTCTGCCGACAGCATAGTACTTGCCTGC 60  
 QY 61 CCAGCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCGGGGCTCCGGAC 120  
 Db 61 CCAGCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTCCGGAC 120  
 QY 121 TGACCTCGCCCTGTCCC 138  
 Db 121 TGACCTCGCCCTGTCCC 138  
 RESULT 10  
 ABN84276  
 ID ABN84276 standard; cDNA; 551 BP.  
 XX AC ABN84276;  
 XX DT 23-SEP-2002 (first entry)  
 XX DE Human neuropeptide Y nucleotide sequence.  
 XX KW Neuropeptide Y; NPY; human; inhibitor; male sexual dysfunction;  
 KW male erectile dysfunction; obesity; anorexia; bulimia; vasotropic;  
 KW anorectic; therapy; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO200247670-A1.  
 XX PD 20-JUN-2002.  
 XX PF 10-DEC-2001; 2001WO-IB002399.  
 XX PR 15-DEC-2000; 2000GB-00030647.  
 PR 06-APR-2001; 2001GB-00008730.  
 PR 23-APR-2001; 2001GB-00009910.  
 PR 04-MAY-2001; 2001GB-00011037.  
 PR 29-JUN-2001; 2001US-00895367.  
 PR 13-JUL-2001; 2001US-00905846.  
 PR 24-AUG-2001; 2001GB-00020679.  
 XX



PA (PFIZ ) PFIZER LTD.  
 PA (PFIZ ) PFIZER INC.  
 XX  
 PI Naylor AM, Van Der Graaf PH, Wayman CP;  
 XX  
 XX WPI; 2002-547828/58.  
 DR  
 XX  
 XX  
 XX Use of an inhibitor of neuropeptide Y in the preparation of medicament  
 PT for the treatment or prevention of male erectile dysfunction.  
 PT  
 XX  
 XX Disclosure; Fig 4; 179pp; English.  
 PS  
 XX  
 XX The present sequence is a human neuropeptide Y (NPY) polynucleotide  
 CC sequence. The invention relates to the use of an inhibitor of NPY, or an  
 CC inhibitor of an NPY Y1 receptor, especially an inhibitor selective for an  
 CC NPY or NPY Y1 receptor associated with male genitalia, in the preparation  
 CC of a medicament for the treatment or prevention of male sexual  
 CC dysfunction, especially male erectile dysfunction (MED). A polypeptide  
 CC encoded by the present sequence may be used as a target in screens to  
 CC identify agents capable of inhibiting NPY. NPY may also be used as a  
 CC target to identify agents capable of mediating an increase in  
 CC intracavernosal pressure through the inhibition of NPY. The inhibitor  
 CC selectively increases intracavernosal pressure of the penis which  
 CC facilitates and/or causes penile erection during sexual arousal. In  
 CC addition to treatment of MED, the inhibitor can also be used to treat  
 CC abnormal drink and food intake disorders, such as obesity, bulimia,  
 CC anorexia and metabolic disorders (all claimed)  
 XX  
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;

Query Match 98.8%; Score 136.4; DB 6; Length 551;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60  
 Db 1 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60

QY 61 CAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCCAGCGGGCTGTCCGGAC 120  
 Db 61 CAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCCAGCGGGCTGTCCGGAC 120

QY 121 TGACCTCGCCCTGTGCC 138  
 Db 121 TGACCTCGCCCTGTGCC 138

RESULT 11  
 AAL47339  
 ID AAL47339 standard; cDNA; 551 BP.  
 XX  
 AC AAL47339;  
 XX  
 XX 18-SEP-2002 (first entry)  
 DT  
 XX  
 XX Human neuropeptide Y coding sequence.  
 DE  
 XX  
 KW Human; neuropeptide Y; NPY; chromosome 7q15.1; SNP; obesity; BMI;  
 KW body mass index; single nucleotide polymorphism; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 PH CDS 87..380  
 FT /\*tag= a  
 FT /product= "NPY"  
 FT 87..170  
 FT sig\_peptide /\*tag= b  
 FT variation replace(106,C)  
 FT /\*tag= d  
 FT 171..380  
 FT mat\_peptide /\*tag= c  
 XX

PN WO200236825-A1.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 02-NOV-2001; 2001WO-SE002431.  
 XX  
 PR 03-NOV-2000; 2000SE-00004035.  
 XX  
 XX (PHAA ) PHARMACIA AB.  
 PA  
 XX  
 PI Wahlestedt C, Ding B;  
 XX  
 XX WPI; 2002-500129/53.  
 DR P-PSDB; AAO18054.  
 DR  
 XX  
 XX Diagnosing single nucleotide polymorphism(s) in the human neuropeptide Y  
 PT (NPY) gene, useful for diagnosing a predisposition to e.g. obesity, by  
 PT determining the nucleic acid sequence at one or more positions of the NPY  
 PT gene in the human.  
 XX  
 XX Example 5; Page 28-29; 37pp; English.  
 PS  
 XX The present invention relates to a method of diagnosing a predisposition  
 CC to obesity in humans by identifying a single nucleotide polymorphism  
 CC (SNP) at position 1128 (position 106 of this sequence) of the  
 CC neuropeptide Y gene. The gene is found at chromosome 7q15.1. The present  
 CC sequence is the NPY coding sequence  
 XX  
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;

Query Match 98.8%; Score 136.4; DB 6; Length 551;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60  
 Db 1 ACCCATCCGCTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60

QY 61 CAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCCAGCGGGCTGTCCGGAC 120  
 Db 61 CAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCCAGCGGGCTGTCCGGAC 120

QY 121 TGACCTCGCCCTGTGCC 138  
 Db 121 TGACCTCGCCCTGTGCC 138

RESULT 12  
 ACF63372  
 ID ACF63372 standard; DNA; 551 BP.  
 XX  
 AC ACF63372;  
 XX  
 XX 09-OCT-2003 (first entry)  
 DT  
 XX  
 XX Human neuropeptide Y gene SEQ ID NO:94.  
 DE  
 XX  
 KW Human; pharmacological; hypotensive; antilipaeamic; vasotropic; laxative;  
 KW dermatological; antidepressant; tranquilliser; antiinflammatory; eczema;  
 KW antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;  
 KW gynaecological; virucide; vulnery; antiarthritic; antipsoriatic; cold;  
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;  
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;  
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;  
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;  
 KW constipation; headache; seizure; multiple sclerosis; polymyositis;  
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;  
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;  
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;  
 KW inflammation; heart burn; infection; colon cancer; malignant melanoma;  
 KW skin disorder; gene; ds.  
 XX  
 OS Homo sapiens.

```
XX WO2003006478-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 10-JUL-2002; 2002WO-US021664.
PF
XX
XX 10-JUL-2001; 2001US-0303820P.
PR
XX
XX (OLIG-) OLIGOS ETC INC.
PA
XX
XX Dale RMK, Arrow A, Thompson T;
PI
XX
XX WPI; 2003-221709/21.
DR
XX
XX Composition with a modified oligonucleotide useful for treating a patient
PT with a pathological disorder such as abnormal appetite, hypertension,
PT eczema, anxiety, stress, and cancer.
XX
XX Claim 6; Page 97; 173pp; English.
PS
XX
XX The present invention describes a composition (I) suitable for
CC administration in a mammal, which comprises a modified oligonucleotide
CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
CC linked by achiral 5'-3' internucleoside phosphate linkages, where the
CC modified oligonucleotide is complementary to a region of a gene
CC associated with a pathological disorder. Also described: (1) a
CC nutritional supplement comprising (II); and (2) a cosmetic composition
CC comprising (II), where the modified oligonucleotide is complementary to a
CC region of a gene associated with a skin disorder. (I) and (II) can have
CC hypotensive, antilipemic, vasotropic, dermatological, antidepressant,
CC tranquilizer, antiinflammatory, antitumor, laxative, antimigraine,
CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
CC vulnary, antiarthritic, antipsoriatic, antimicrobial, cytostatic and
CC litholytic activities. (I) can be used for treating a patient with a
CC pathological disorder selected from abnormal appetite, hypertension,
CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,
CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
CC chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,
CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant
CC melanoma, and malignant nasal polyps. The nutritional supplement is
CC useful for supplementing the diet of an individual, and the cosmetic
CC composition is useful for improving the appearance of the skin in an
CC individual with a skin disorder. ACF63279 to ACF63410 represent
CC nucleotide sequence given in the exemplification of the present invention
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
SQ
Query Match 98.8%; Score 136.4; DB 7; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.7e-29;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACCCATCGCTGGTCTCACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCG 60
DB 1 ACCCATCGCTGGTCTCACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCG 60
QY 61 CCAGCCACCGCGCGCGCAGCACCATCTAGGTAAACAGCGACCGGGGCTGTCCGAC 120
DB 61 CCAGCCACCGCGCGCGCAGCACCATCTAGGTAAACAGCGACTTGGGGCTGTCCGAC 120
QY 121 TGACCCCTCGCCCTGTCTCC 138
DB 121 TGACCCCTCGCCCTGTCTCC 138
RESULT 13
AAF72746
ID AAF72746 standard; cDNA; 969 BP.
XX
```

```
AC AAF72746;
XX
XX 24-APR-2001 (first entry)
XX
XX Human prostate cancer antigen coding sequence #6.
XX
XX Immunosuppressive; nootropic; neuroprotective; antiviral; vulnary;
KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
KW immune disorder; cardiovascular disorder; neurological disease;
KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
KW antiasthmatic; anticonvulsant; vasotropic; vulnary; human;
KW secreted protein; prostate cancer antigen; ss.
XX
XX Homo sapiens.
OS
XX WO200107476-A1.
PN
XX 01-FEB-2001.
PD
XX
XX 20-JUL-2000; 2000WO-US019666.
PF
XX
XX 21-JUL-1999; 99US-0144972P.
PR
XX 13-AUG-1999; 99US-0148681P.
PR
XX 17-AUG-1999; 99US-0149173P.
PR
XX 06-OCT-1999; 99US-0158004P.
PR
XX 05-APR-2000; 2000US-0194689P.
XX
XX (HUWA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Rosen CA, Birse C;
PI
XX WPI; 2001-138554/14.
DR P-PSDB; AAB80278.
XX
XX New nucleic acid molecule encoding human secreted prostate cancer
PT antigens, useful for the diagnosis and treatment of disorders such as
PT cancer, leukemia and autoimmune disease.
XX
XX Claim 1; Page 359-360; 433pp; English.
XX
XX The present invention relates to human secreted prostate cancer antigen
CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
CC The coding sequences and proteins of the present invention are useful for
CC preventing, treating or ameliorating a medical condition; and for the
CC diagnosis and treatment of diseases and disorders. Diseases and disorders
CC that can be diagnosed and treated include (auto)immune diseases (e.g.
CC graft versus host disease and rheumatoid arthritis), inflammatory and
CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
CC neurological disorders (e.g. Alzheimer's Parkinson's disease, epilepsy
CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
CC viruses or parasites. They may also be useful for wound healing,
CC epithelial cell proliferation, supporting cell culture, tissue
CC regeneration, birth control and as a food additive or preservative. The
CC coding sequences can be used to generate fusion proteins by linking the
CC coding sequences to the human immunoglobulin G Fc portion coding sequence
CC (AAF72732) for increasing the stability of the fusion protein as compared
CC to the human protein only
XX
XX Sequence 969 BP; 246 A; 275 C; 225 G; 210 T; 0 U; 13 Other;
SQ
Query Match 89.3%; Score 123.2; DB 4; Length 969;
Best Local Similarity 96.2%; Pred. No. 1.5e-25;
Matches 125; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 9 CGCTGGCTCTACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCGCCGCCAC 69
DB 250 CGAGNNCTCTACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCGCCGCCAC 309
```



CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention

XX  
 SQ Sequence 599 BP; 163 A; 169 C; 139 G; 120 T; 0 U; 8 Other;

Query Match 79.3%; Score 109.4; DB 3; Length 599;  
 Best Local Similarity 98.4%; Pred. No. 1.2e-21;  
 Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 16 TCTCACCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGCCTCGCCCGACGCGCCGCG 75

Db 14 TCTCACCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGCCTCGCCCGACGCGCCGCG 73

Qy 76 CGCCAGCCACCATGCTAGGTAAACAGCGACCGGGGCTGTCCGGACTGACCCCTCGCCCTGT 135

Db 74 CGCCA-CCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTGT 132

Qy 136 CCC 138

Db 133 CCC 135

Search completed: April 26, 2004, 14:04:43  
 Job time : 272 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 2161 Seconds  
(without alignments)  
1906.979 Million cell updates/sec

Title: US-09-645-590-2

Perfect score: 138

Sequence: 1 accccatccgctgctctca.....actgacccctgcctgtccc 138

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136.4	98.8	463	14	CA772698
2	136.4	98.8	584	12	BI457963
3	136.4	98.8	873	13	BU930481
4	135.4	98.1	300	9	AU100303

5	133.4	96.7	136	9	AU077324
6	126.4	91.6	521	9	AI879081
7	125.4	90.9	556	13	BQ721485
8	125.4	90.9	557	13	BQ925183
9	125.4	90.9	963	13	BQ876913
c 10	124.8	90.4	550	9	A1928896
c 11	123.8	89.7	544	9	A1826374
12	123.4	89.4	468	13	EX101548
13	122.4	88.7	433	9	AI929147
14	112.4	81.4	567	13	BQ932266
15	105.2	76.2	1123	13	BQ886097
16	87	63.0	766	13	BU930120
17	85	61.6	1695	10	BF680552
c 18	78.4	56.8	498	9	AI199681
19	69.4	50.3	424	9	AA061961
20	69.4	50.3	443	9	AI385504
21	69.4	50.3	492	13	BX527459
22	69.4	50.3	556	11	AK002982
23	69.4	50.3	585	13	BU937569
24	69.4	50.3	591	13	BU558492
25	69.4	50.3	600	13	BU604192
26	69.4	50.3	926	13	BU936355
27	68	49.3	489	10	BE653691
28	68	49.3	493	13	BQ84972
c 29	68	49.3	534	13	BQ084688
30	68	49.3	569	13	BQ564644
c 31	66.8	48.4	574	9	AI198311
32	64.6	46.8	435	14	CB792893
33	61.6	44.6	402	14	CB769232
34	61.6	44.6	520	12	BG684369
35	61.6	44.6	529	14	CB719328
36	61.6	44.6	544	14	CB612099
c 37	61.6	44.6	587	14	CB585333
38	61.4	44.5	408	9	AA270394
39	61.4	44.5	483	14	W70782
40	60.6	43.9	570	12	BQ044605
41	60	43.5	364	13	BQ290146
42	55	39.9	454	14	CB741987
43	55	39.9	461	14	CB736748
44	55	39.9	499	14	CB712314
45	55	39.9	500	14	CB712006

## ALIGNMENTS

RESULT 1

CA772698

LOCUS

DEFINITION

CA772698 463 bp mRNA linear EST 03-DEC-2002

1083901.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6133056 5'

similar to SW:NEUY\_HUMAN P01303 NEUROPEPTIDE Y PRECURSOR ; , mRNA

sequence.

CA772698

CA772698.1 GI:26009965

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

REFERENCE

1 (bases 1 to 463)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Leimishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Haller, L., Ma, M., Pape, D., Wylie, T., Martin, J., Blustein, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,

Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: i083901.xl

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmeiton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)

Putative full length read

vector to vector length is 598

Seq primer: -40RP from Gibco.

Location/Qualifiers

1. 463

/organism="Homo sapiens"

/mol\_type="rRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6133056"

/tissue type="Purified pancreatic islet"

/lab host="DH10B"

/clone lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:

NotI; Site\_2: XhoI; cDNA made by oligo-dT priming. ~1kb. 5'

Size-selected on agarose gel. Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD,

Metabolism Div. (Alan Permutt Lab), Washington University

School of Medicine, Box 8127, 660 South Euclid Ave., St.

Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:

314-362-1916, Fax: 314-747-2692."

## FEATURES

source

http://image.llnl.gov

Plate: L1AM11703 row: 0 column: 13

High quality sequence stop: 584.

Location/Qualifiers

source

1. 584

/organism="Homo sapiens"

/mol\_type="rRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5278692"

/tissue type="hypothalamus"

/lab host="DH10B"

/clone lib="NIH\_MGC\_96"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTVN-3', size-selected for average

insert size 2.3 kb and normalized to 80T 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH\_MGC Library."

## ORIGIN

Query Match 98.8%; Score 136.4; DB 12; Length 584;

Best Local Similarity 99.3%; Pred. No. 3.1e-23;

Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## ORIGIN

Query Match 98.8%; Score 136.4; DB 14; Length 463;

Best Local Similarity 99.3%; Pred. No. 2.9e-23;

Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGGTGGCTCTCACCCCTGGAGAGCGTGGCCGACAGCATAGTACTTGCCGC 60

|||||

Db 28 ACCCATCGGTGGCTCTCACCCCTGGAGAGCGTGGCCGACAGCATAGTACTTGCCGC 87

|||||

QY 61 CCAGCCACGCCCGCGCGCCAGCACCATGCTAGGTAACAAGCGACCGGGCTGTCGGAC 120

|||||

Db 89 CCAGCCACGCCCGCGCGCCAGCACCATGCTAGGTAACAAGCGACTGGGGCTGTCGGAC 147

|||||

QY 121 TGACCTCGCCCTGTGCC 138

|||||

Db 148 TGACCTCGCCCTGTGCC 165

|||||

## RESULT 2

BI457963

LOCUS

BI457963 603198956F1 NIH\_MGC\_96 584 bp mRNA linear EST 21-AUG-2001

DEFINITION

mRNA sequence.

ACCESSION

BI457963

VERSION

BI457963.1 GI:15248619

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 584)

AUTHORS

NIH-MGC http://imgc.ncbi.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Inyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

## RESULT 3

BU930481

LOCUS

DEFINITION

AGENCOURT 10424773 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:6668512

5', mRNA sequence.

ACCESSION

BU930481

VERSION

BU930481.1 GI:24119300

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 873)

AUTHORS

NIH-MGC http://imgc.ncbi.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: CLONTECH

cDNA Library Preparation: CLONTECH

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM2942 row: 1 column: 16

High quality sequence stop: 510.

Location/Qualifiers

source

1. 873

/organism="Homo sapiens"

/mol\_type="rRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6668512"  
 /lab host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_83"  
 /notes="Organ: prostate; Vector: pDNR-LIB (Clontech);  
 Site 1: Sfil (ggcgctctggcc); Site 2: Sfil  
 (ggccattatggcc); 5' and 3' adaptors were used in cloning  
 as follows: 5' adaptor sequence: 5'-CAGGGCCATTATGCCG-3'  
 and 3' adaptor sequence:  
 5'-ATTCTAGGCGGAGGGGGCGGACATG-dT(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.4  
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA)."

## ORIGIN

Query Match 99.8%; Score 136.4; DB 13; Length 873;  
 Best Local Similarity 99.3%; Pred. No. 3.4e-23;  
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ACCCATCCGCTGGCTCTCAACCTCGGAGCGCTCGCCGACAGCATAGTACTTGC CGC 60  
 Db 4 ACCCATCCGCTGGCTCTCAACCTCGGAGCGCTCGCCGACAGCATAGTACTTGC CGC 63  
 QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAAGCGACCGGGCTGTCCGGAC 120  
 Db 64 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAAGCGACTGGGGCTGTCCGGAC 123  
 QY 121 TGACCTTCGCCCTGTCCC 138  
 Db 124 TGACCTTCGCCCTGTCCC 141

## RESULT 4

AU100303  
 LOCUS 300 bp mRNA linear EST 05-APR-2001  
 DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 Zrv6c665 similar to Human neuro peptide Y (NPY) mRNA, mRNA sequence.  
 ACCESSION AU100303  
 VERSION AU100303  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 300)  
 AUTHORS Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S.,  
 Okubo, K., Suyama, A. and Sugano, S.  
 In silico mapping of the 5'-ends of human mRNAs using full-length  
 enriched and 5'-end enriched cDNA libraries constructed by  
 Oligo-capping method  
 Unpublished (2001)  
 CONTACT: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

## TITLE

## JOURNAL

## COMMENT

## FEATURES

source  
 1. .300  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="Zrv6c665"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 98.1%; Score 135.4; DB 9; Length 300;  
 Best Local Similarity 98.6%; Pred. No. 4.6e-23;

Matches 136; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ACCCATCCGCTGGCTCTCAACCTCGGAGCGCTCGCCGACAGCATAGTACTTGC CGC 60  
 Db 1 ACCCATCCGCTGGCTCTCAACCTCGGAGCGCTCGCCGACAGCATAGTACTTGC CGC 60  
 QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAAGCGACCGGGCTGTCCGGAC 120  
 Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCTTCGCCCTGTCCC 138  
 Db 121 TGACCTTCGCCCTGTCCC 138

## RESULT 5

AU077324  
 LOCUS 136 bp mRNA linear EST 04-MAY-2000  
 DEFINITION Sugano cDNA library Homo sapiens cDNA clone Zrv6c665  
 similar to 5'-end region of Human neuro peptide Y (NPY) mRNA, mRNA  
 sequence.  
 ACCESSION AU077324  
 VERSION AU077324  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 136)  
 AUTHORS Suzuki, Y., Ishihara, D., Sasaki, M., Nakagawa, H., Hata, H.,  
 Tsunoda, T., Watanabe, M., Komatsu, T., Ota, T., Isogai, T., Suyama, A.  
 and Sugano, S.  
 Statistical analysis of the 5' untranslated region of human mRNA  
 using 'Oligo-Capped' cDNA libraries  
 Genomics 64 (3), 286-297 (2000)

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997)

This clone was obtained from a '5'-end-enriched' cDNA library  
 constructed by 'Oligo-Capping' method. The coding region starts  
 from the 50 bp upstream to the 3'-end.

## FEATURES

## source

1. .136  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="Zrv6c665"  
 /clone\_lib="Sugano cDNA library"

## ORIGIN

Query Match 96.7%; Score 133.4; DB 9; Length 136;  
 Best Local Similarity 98.5%; Pred. No. 1.2e-22;  
 Matches 134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCAACCTCGGAGCGCTCGCCGACAGCATAGTACTTGC CGC 60  
 Db 1 ACCCATCCGCTGGCTCTCAACCTCGGAGCGCTCGCCGACAGCATAGTACTTGC CGC 60  
 QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAAGCGACCGGGCTGTCCGGAC 120  
 Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAAGCGACTGGGGCTGTCCGGAC 120  
 QY 121 TGACCTTCGCCCTGTCC 136  
 Db 121 TGACCTTCGCCCTGTCC 136

```

RESULT 6
AI879081      521 bp      mRNA      linear      EST 23-AUG-1999
LOCUS      aus4b11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
DEFINITION      IMAGE:2518557 5', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
              (HUMAN);, mRNA sequence.
ACCESSION      AI879081      GI:5553130
VERSION      AI879081.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 521)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
              Krizman,D., McCabe,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
              Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
              Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
              WashU-NCI human EST Project
              Unpublished (1997)
              Other ESTs: aus4b11.x1
              Contact: Wilson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Seq primer: -40RP from Gibco
              High quality sequence stop: 425.
FEATURES      source
              location/Qualifiers
              1..521
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:2518557"
               /sex="male"
               /tissue_type="frontal lobe"
               /dev_stage="5 months post-conception"
               /lab_host="DH10B"
               /clone_lib="Schneider fetal brain 00004"
               /note="Organ: brain; Vector: pBluescript SK (Stratagene);
              Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was
              prepared from human fetal brain tissue. 5' and 3'
              adaptors were used in cloning as follows: 5' adaptor
              sequence:
              5'-GAGAGAGAGAGAGCTCAAGGATCTCTTAATTAATTAATCCCGCCCGCC-3',
              and 3' adaptor sequence:
              5'-GAGAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was
              size-selected for >0.5 kb inserts and has an average
              insert size estimated at 1.2 kb. This library was
              constructed using the CAP-trapper method for full-length
              enrichment and has not undergone amplification. Library
              was constructed by Dr. Claudio Schneider (INCI-B-Area
              Science Park, Trieste, Italy)."
ORIGIN
Query Match      91.6%; Score 126.4; DB 9; Length 521;
Best Local Similarity 99.2%; Pred. No. 8.1e-21;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      11      CTGGCTCTACCCCTCGGAGAGCTCGCCGACAGATAGTACTTCGCCGCCAGCCAGCC 70
              |||||
Db      1      CTGGCTCTACCCCTCGGAGAGCTCGCCGACAGATAGTACTTCGCCGCCAGCCAGCC 60
              |||||
QY      71      CCSCGCGCCAGCCACCACCTAGGTAAACAGGACCGGGGCTGTCCGGACTGACCTCGC 130
              |||||
Db      61      CCSCGCGCCAGCCACCACCTAGGTAAACAGGACCTGGGGCTGTCCGGACTGACCTCGC 120
              |||||
QY      131      CCTGTCCC 138
              |||||

```

```

Db      121      CCTGTCCC 128
              |||||
RESULT 7
BQ721485
LOCUS      BQ721485      556 bp      mRNA      linear      EST 16-JUL-2002
DEFINITION      AGNCOURT 8234409 Lupski synepathetic_trunk Homo sapiens cDNA clone
              IMAGE:6188546 5', mRNA sequence.
ACCESSION      BQ721485
VERSION      BQ721485.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 556)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabs-remail.nih.gov
              Tissue Procurement: Dr. James R. Lupski
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLM1584 row: f column: 03
              High quality sequence stop: 555.
FEATURES      source
              location/Qualifiers
              1..556
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:6188546"
               /sex="male"
               /tissue_type="sympathetic trunk"
               /dev_stage="adult, 16 yr"
               /lab_host="DH10B"
               /clone_lib="Lupski synepathetic trunk"
               /note="Vector: pCMW-SPORT6 (life technologies); Site_1:
              NotI; Site_2: SalI; cDNA made by oligo-dT priming.
              Directionally cloned using the following adaptors:
              5'-TCGACCCAGCGCTCGC-3' and
              5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
              1 kb for average insert length 1.9 kb. This is a primary
              library, non-amplified. Library constructed by Life
              Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
              College of Medicine); available through Life
              Technologies."
ORIGIN
Query Match      90.9%; Score 125.4; DB 13; Length 556;
Best Local Similarity 99.2%; Pred. No. 1.4e-20;
Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      12      TGCGTCTCACCCCTCGGAGAGCTCGCCGACAGATAGTACTTCGCCGCCAGCCAGCC 71
              |||||
Db      1      TGCGTCTCACCCCTCGGAGAGCTCGCCGACAGATAGTACTTCGCCGCCAGCCAGCC 60
              |||||
QY      72      CGCGCGCCAGCCACCACCTAGGTAAACAGGACCGGGGCTGTCCGGACTGACCTCGCC 131
              |||||
Db      61      CGCGCGCCAGCCACCACCTAGGTAAACAGGACCTGGGGCTGTCCGGACTGACCTCGCC 120
              |||||
QY      132      CTGTCCC 138
              |||||
Db      121      CTGTCCC 127
              |||||
RESULT 8
BQ25183

```



**LOCUS** BQ925183 557 bp mRNA linear EST 20-AUG-2002  
**DEFINITION** AGENCOURT 8821446 Lupski\_sciatic nerve Homo sapiens cDNA clone  
**IMAGE:**6203754 5', mRNA sequence.  
**ACCESSION** BQ925183  
**VERSION** BQ925183.1 GI:22340214  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 557)  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM13623 row: o column: 19  
 High quality sequence stop: 556.  
**FEATURES** Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6203754"  
 /sex="male"  
 /tissue\_type="sciatic nerve"  
 /dev\_stage="adult, 70 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski sciatic nerve"  
 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACCGCTCCG-3' and  
 5'-GACTAGTTCTAGATCGGAGCGCTGCGGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.87 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."  
**ORIGIN**  
 Query Match 90.9%; Score 125.4; DB 13; Length 557;  
 Best Local Similarity 99.2%; Pred. No. 1.4e-20;  
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 TGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGCCAGCCAGCC 71  
 Db 1 TGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGCCAGCCAGCC 60  
 QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCGGACTGACCCCTGCC 131  
 Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCGGACTGACCCCTGCC 120  
 QY 132 CTGTCCC 138  
 Db 121 CTGTCCC 127  
**RESULT** 9  
**LOCUS** BQ876913 963 bp mRNA linear EST 16-AUG-2002  
**DEFINITION** AGENCOURT 8417678 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone  
**IMAGE:**6193004 5', mRNA sequence.  
**ACCESSION** BQ876913  
**VERSION** BQ876913.1 GI:22268921  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 963)  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM13623 row: o column: 19  
 High quality sequence stop: 556.  
**FEATURES** Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6193004"  
 /sex="male"  
 /tissue\_type="sympathetic trunk"  
 /dev\_stage="adult, 16 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski sympathetic trunk"  
 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACCGCTCCG-3' and  
 5'-GACTAGTTCTAGATCGGAGCGCTGCGGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."  
**ORIGIN**  
 Query Match 90.9%; Score 125.4; DB 13; Length 963;  
 Best Local Similarity 99.2%; Pred. No. 1.6e-20;  
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 TGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGCCAGCCAGCC 71  
 Db 1 TGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGCCAGCCAGCC 60  
 QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCGGACTGACCCCTGCC 131  
 Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCGGACTGACCCCTGCC 120  
 QY 132 CTGTCCC 138  
 Db 121 CTGTCCC 127  
**RESULT** 10  
**LOCUS** AI928896/c 550 bp mRNA linear EST 23-AUG-1999  
**DEFINITION** au65f07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone  
**IMAGE:**2519653 3', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR  
 (HUMAN); mRNA sequence.  
**ACCESSION** AI928896  
**VERSION** AI928896.1 GI:5664860  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 550)

**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 963)  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM13595 row: o column: 21  
 High quality sequence stop: 517.  
**FEATURES** Location/Qualifiers  
 source  
 1..963  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6193004"  
 /sex="male"  
 /tissue\_type="sympathetic trunk"  
 /dev\_stage="adult, 16 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski sympathetic trunk"  
 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACCGCTCCG-3' and  
 5'-GACTAGTTCTAGATCGGAGCGCTGCGGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."  
**ORIGIN**  
 Query Match 90.9%; Score 125.4; DB 13; Length 963;  
 Best Local Similarity 99.2%; Pred. No. 1.6e-20;  
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 TGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGCCAGCCAGCC 71  
 Db 1 TGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGCCAGCCAGCC 60  
 QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCGGACTGACCCCTGCC 131  
 Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCGGACTGACCCCTGCC 120  
 QY 132 CTGTCCC 138  
 Db 121 CTGTCCC 127  
**RESULT** 10  
**LOCUS** AI928896/c 550 bp mRNA linear EST 23-AUG-1999  
**DEFINITION** au65f07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone  
**IMAGE:**2519653 3', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR  
 (HUMAN); mRNA sequence.  
**ACCESSION** AI928896  
**VERSION** AI928896.1 GI:5664860  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 550)

AUTHORS  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Joest, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,  
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 TITLE  
 WashU-NCI human EST Project  
 JOURNAL  
 Unpublished (1997)  
 COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 481.

```

FEATURES
source
1. .550
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2519653"
/sex="male"
/tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
/clone_lib="Schneider fetal brain 00004"
/note="Organ: brain; Vector: pBluescript SK (Stratagene);
Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence:
5'-GAGAGAGAGAGAGCTCAAGATCCTTAATTAATATCCCCCCCCCCCC-3'
and 3' adaptor sequence:
5'-GAGAGAGAGAGCTCAGATTTTTTTTTTTTTTTT-3'. The library was
size-selected for >0.5 kb inserts and has an average
insert size estimated at 1.2 kb. This library was
constructed using the CAP-trapper method for full-length
enrichment and has not undergone amplification. Library
was constructed by Dr. Claudio Schneider (LNCIB-Area
Science Park, Trieste, Italy). "

```

[illegible]

RESULT 11  
AI826374/c  
LOCUS  
DEFINITION  
AI826374  
544 bp mRNA linear EST 07-MAR-2000  
w44912.x1 NCI CGAP Pr-22 Homo sapiens cDNA clone IMAGE:2418310 3'  
similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR (HUMAN);; mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p>	<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p>

## ORIGIN

	Query Match	89.7%;	Score 123.8;	DB 9;	Length 544;
	Best local Similarity	98.4%;	Pred. No. 3.5e-20;		
	Matches 125;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	12	TGCGCTTCACCCCTCGGAGACGCTCGCCGACGACATAGTACTTCGCCGCCAGCCACGCC	71		
Db	544	TGCGCTTCACCCCTCGGAGACGCTCGCCGACGACATAGTACTTCGCCGCCAGCCACGCC	485		
Qy	72	CGCGCGCGACGCCACCATGCTAGGTAAACAAGCGACCGGGGCTGTCGGGACTGACCCCTCGCC	131		
Db	484	CGCGCGCGACGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCGGGACTGACCCCTCGCC	425		
Qy	132	CTGTCC	138		
Db	424	CTGTCC	418		

RESULT 12	EX101548	468 bp	mRNA	linear	EST 06-FEB-2003
LOCUS	EX101548				
DEFINITION	EX101548 Soares placenta 8c9weeks 2NDHP8to9W Homo sapiens CDNA clone IMAGE998K074642 ; IMAGE:1894398, mRNA sequence.				
ACCESSION	EX101548				
VERSION	EX101548.1	GI:27844953			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 468)				
AUTHORS	Eberl, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Raderhof, U., Schneider, D. and Korn, B.				
TITLE	Human Unigeneset - RZPD3				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Ina Rolf				

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998K074642.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
<http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972> Contact: Ina Rofls  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)

This clone is available royalty-free from RZPD;  
contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
M13r, Primer sequence: TTTACACAGGAACACGATGAC.

## FEATURES

source

```
1. .468
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clones="IMAGp998K074642 ; IMAGE:1894398"
  /dev_stage="two placentae: one from 8 weeks and another
  from 9 weeks post conception"
  /lab_host="DH10B (ampicillin resistant)"
  /clone_lib="Soares_Placenta 8to9weeks 2NBP8to9W"
  /note="Organ: Placenta; Vector: p7713D (Pharmacia) with a
  modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
  strand cDNA was primed with a Not I - oligo(dT) primer [5'
  TGTACCAATCTGAAGTGGAGCGCGCGATTTTATTTTATTTT 3'],
  double-stranded cDNA was size selected, ligated to Eco RI
  adapters (Pharmacia), digested with Not I and cloned into
  the Not I and Eco RI sites of a modified p7713 vector
  (Pharmacia). Library constructed by Bento Soares and
  M.Fatima Bonaldo."
```

## ORIGIN

```
Query Match      89.4%; Score 123.4; DB 13; Length 468;
Best Local Similarity 99.2%; Pred. No. 4.2e-20;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GCTCTACCCCTCGGAGACGCTGCCCGACAGCATAGTACTTGGCCGCCAGCCAGCCGC 73
|||||
Db 1 GCTCTACCCCTCGGAGACGCTGCCCGACAGCATAGTACTTGGCCGCCAGCCAGCCGC 60

QY 74 CGCGCCAGCCACCATGTAGTAAACAGCAGCGGGGCTGTCCGACTGACCCCTGCCCT 133
|||||
Db 61 CGCGCCAGCCACCATGTAGTAAACAGCAGCTGGGGCTGTCCGACTGACCCCTGCCCT 120

QY 134 GTCCC 138
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Db 121 GTCCC 125
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## RESULT 13

AI929147

LOCUS

```
AI929147      433 bp      mRNA      linear      EST 23-AUG-1999
au65f07.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2519653 5' similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
(HUMAN); mRNA sequence.
```

## ACCESSION

AI929147

VERSION

AI929147.1

GI:5665111

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 433)

Haller L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,

Krizman J., Moore B., Lacy M., Lennon G., Marra M.,

Martin J., White Y., Whillie T., Waterston R. and Wilson R.

WashU-NCI human EST Project

Unpublished (1997)

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40RP from Gibco.

## FEATURES

source

```
1. .433
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clones="IMAGE:2519653"
  /sex="male"
  /tissue_type="frontal lobe"
  /dev_stage="5 months post-conception"
  /lab_host="DH10B"
  /clone_lib="Schneider fetal brain 00004"
  /note="Organ: brain; Vector: pBluescript SK (Stratagene);
  Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was
  prepared from human fetal brain tissue. 5' and 3'
  adaptors were used in cloning as follows: 5' adaptor
  sequence:
  5'-GAGAGAGAGAGAGCTCAAGGATCTTTAATTAAATTCCTCCCTCCCTCC-3'
  and 3' adaptor sequence:
  5'-GAGAGAGAGAGCTGAGTTTATTTTATTTT-3'. The library was
  size-selected for >0.5 kb inserts and has an average
  insert size estimated at 1.2 kb. This library was
  constructed using the CAP-trapper method for full-length
  enrichment and has not undergone amplification. Library
  was constructed by Dr. Claudio Schneider (LNCIB-Area
  Science Park, Trieste, Italy)."
```

## ORIGIN

```
Query Match      88.7%; Score 122.4; DB 9; Length 433;
Best Local Similarity 99.2%; Pred. No. 7.3e-20;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTCTACCCCTCGGAGACGCTGCCCGACAGCATAGTACTTGGCCGCCAGCCAGCCGC 74
|||||
Db 1 CTCTACCCCTCGGAGACGCTGCCCGACAGCATAGTACTTGGCCGCCAGCCAGCCGC 60

QY 75 CGCCAGCCACCATGCTAGGTAAACAGCAGCGGGGCTGTCCGACTGACCCCTGCCCTG 134
|||||
Db 61 CGCCAGCCACCATGCTAGGTAAACAGCAGCTGGGGCTGTCCGACTGACCCCTGCCCTG 120

QY 135 TCCC 138
|||||
Db 121 TCCC 124
```

## RESULT 14

BQ932266

LOCUS

```
BQ932266      567 bp      mRNA      linear      EST 21-AUG-2002
AGENCOURT 8804926 Lupeki sciatic nerve Homo sapiens cDNA clone
IMAGE:6197017 5', mRNA sequence.
```

## ACCESSION

BQ932266

VERSION

BQ932266.1

GI:22347297

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 567)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Cloning Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM13606 row: g column: 02  
 High quality sequence stop: 566.

# FEATURES

Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:6197017"  
 /sex="male"  
 /tissue\_type="sciatic nerve"  
 /dev\_stage="adult, 70 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski sciatic nerve"  
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACGGCTCCG-3' and  
 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.87 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

# ORIGIN

Query Match 81.4%; Score 112.4; DB 13; Length 567;  
 Best Local Similarity 99.1%; Pred. No. 2.1e-17;  
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 25 TCGGAGACGTCGCCCGCAGCATAGTACTTCCGCCCGCAGCAGCCCGCGCCAGCCA 84  
 Db 1 TCGGAGACGTCGCCCGCAGCATAGTACTTCCGCCCGCAGCAGCCCGCGCCAGCCA 60  
 QY 85 CCATCTAGGTAACAAGCGCGGCTGTCGGAGTACCTCGCCCTGTCCTCC 138  
 Db 61 CCATCTAGGTAACAAGCGCGCTGGGGCTGTCCGGAGTACCTCGCCCTGTCCTCC 114

# RESULT 15

B0886097  
 LOCUS 1123 bp mRNA linear EST 16-AUG-2002  
 DEFINITION AGENCOURT\_8673508 Lupski\_sciatic\_nerve Homo sapiens cDNA clone  
 IMAGE:6199943 5', mRNA sequence.  
 B0886097  
 B0886097.1 GI:22278111  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1123)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
 Tissue Procurement: Dr. James R. Lupski  
 cdna Library Preparation: Life Technologies, Inc.  
 cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM13613 row: p column: 24  
 High quality sequence start: 90  
 High quality sequence stop: 266.

# FEATURES

Location/Qualifiers  
 1..1123

source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6199943"  
 /sex="male"  
 /tissue\_type="sciatic nerve"  
 /dev\_stage="adult, 70 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski sciatic nerve"  
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACGGCTCCG-3' and  
 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.87 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

# ORIGIN

Query Match 76.2%; Score 105.2; DB 13; Length 1123;  
 Best Local Similarity 89.9%; Pred. No. 1.4e-15;  
 Matches 124; Conservative 0; Mismatches 13; Indels 1; Gaps 1;  
 QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGCAGCATAGTACTTGGCGC 60  
 Db 41 ACCGCCACGCGTCCGCTCACCCCTCGGAGACGCTCGCCCGCAGCATAGTACTCGACGC 99  
 QY 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGCGGGCTGTCCGGAC 120  
 Db 100 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGGGCTGTCCGGAC 159  
 QY 121 TGACCCCTCGCCCTGTCCC 138  
 Db 160 TGACCCCTCGCCCTGTCCC 177

Search completed: April 26, 2004, 15:45:52  
 Job time : 2161 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 59.5 Seconds  
(without alignments)  
1287.113 Million cell updates/sec

Title: US-09-645-590-2

Perfect score: 138

Sequence: 1 accccatcgctggctctca.....actgacctgcctgtccc 138

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

1: /cgn2\_6/prodata/2/ina/5A COMB.seq.\*

2: /cgn2\_6/prodata/2/ina/5B COMB.seq.\*

3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*

4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*

5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq.\*

6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	1588	4	US-09-976-594-625
2	136.4	98.8	551	3	US-08-994-946A-5
3	136.4	98.8	551	4	US-09-291-994-5
4	111.6	80.9	122	4	US-09-621-976-8234
5	89.4	64.8	325	3	US-08-994-946A-1
6	89.4	64.8	325	4	US-09-291-994-1
7	50.4	36.5	247	3	US-08-994-946A-2
8	50.4	36.5	247	4	US-09-291-994-2
9	32.2	23.3	945	4	US-09-252-991A-14797
10	32.2	23.3	2550	4	US-09-252-991A-14954
11	31.8	23.0	1242	4	US-09-252-991A-9668
12	31.8	23.0	1521	4	US-09-252-991A-9746
13	31.8	23.0	1521	4	US-09-252-991A-9494
14	31.8	23.0	2583	4	US-09-252-991A-9541
15	31.2	22.6	999	4	US-09-252-991A-14871
16	31.2	22.6	1608	4	US-09-252-991A-14871
17	30.8	22.3	1108	4	US-09-800-729-42
18	30.8	22.3	1141	4	US-09-800-729-78
19	30.8	22.3	1297	4	US-09-800-729-80
20	30.2	21.9	1518	4	US-09-489-039A-6357
21	30	21.4	1546	4	US-09-383-318A-1
22	29.6	21.4	480	4	US-09-674-608A-4
23	29.2	21.2	576	4	US-09-252-991A-7331
24	29.2	21.2	670	4	US-09-009-816-3
25	29.2	21.2	1104	4	US-09-009-816-1
26	29.2	21.2	1302	4	US-09-252-991A-7221
27	29.2	21.2	1551	4	US-09-252-991A-7473

28	29.2	21.2	1578	4	US-09-252-991A-7410	Sequence 7410, Ap
c 29	29	21.0	411	4	US-09-252-991A-8321	Sequence 8321, Ap
30	29	21.0	783	4	US-09-252-991A-8452	Sequence 8452, Ap
c 31	29	21.0	966	4	US-09-252-991A-8354	Sequence 8354, Ap
c 32	29	21.0	1110	4	US-09-252-991A-8388	Sequence 8388, Ap
c 33	29	21.0	1131	4	US-09-252-991A-8486	Sequence 8486, Ap
c 34	29	21.0	3638	4	US-09-369-364A-8	Sequence 8, Appli
c 35	28.8	20.9	807	4	US-09-489-039A-5230	Sequence 5230, Ap
c 36	28.6	20.7	804	4	US-09-252-991A-15809	Sequence 15809, A
c 37	28.6	20.7	2073	4	US-09-252-991A-15779	Sequence 15779, A
c 38	28.6	20.7	3664	1	US-07-880-913-1	Sequence 1, Appli
c 39	28.4	20.6	279	4	US-09-252-991A-8120	Sequence 8120, Ap
40	28.4	20.6	735	4	US-09-252-991A-8185	Sequence 8185, Ap
41	28.4	20.6	1247	1	US-08-278-729A-32	Sequence 32, Appl
42	28.4	20.6	1247	1	US-08-155-343A-32	Sequence 32, Appl
43	28.4	20.6	1247	1	US-08-406-672-32	Sequence 32, Appl
44	28.4	20.6	1247	1	US-08-643-563A-32	Sequence 32, Appl
45	28.4	20.6	1247	1	US-08-643-763A-32	Sequence 32, Appl

#### ALIGNMENTS

RESULT 1  
US-09-976-594-625  
; Sequence 625, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchbinder, Jenny  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 625  
; LENGTH: 1588  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6673549 1344185CB1  
; NAME/KEY: unsure  
; LOCATION: 7, 19, 25, 32, 45, 59, 88, 96, 108, 116, 124, 150, 167, 181, 191, 216,  
; LOCATION: 221, 226, 233, 246, 264, 276, 286, 303, 307, 315, 330, 332, 336, 351, 359,  
; LOCATION: 363, 373, 377, 382, 395, 407, 424, 431, 435, 442, 446, 470, 488, 492, 499,  
; LOCATION: 504, 537, 551, 556, 583, 592, 596, 604, 615, 641, 671, 696, 709, 714, 726,  
; LOCATION: 738, 747, 751, 756, 762, 774, 810, 842, 844, 906  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-976-594-625

Query Match 100.0%; Score 138; DB 4; Length 1588;  
Best Local Similarity 100.0%; Pred. No. 1.5e-31;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTATTGCGGC 60  
Db 1031 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTATTGCGGC 1090

QY 61 CCAGCCAGCCCGCGCCGACGATCTAGTAAAGCGACCGGGGCTGTCCGGAC 120  
Db 1091 CCAGCCAGCCCGCGCCGACGATCTAGTAAAGCGACCGGGGCTGTCCGGAC 1150  
QY 121 TGACCTCGCCCTGTCCC 138  
Db 1151 TGACCTCGCCCTGTCCC 1168

RESULT 2  
US-08-994-946A-5

; Sequence 5, Application US/08994946A  
; Patent No. 6046317  
; GENERAL INFORMATION:  
; APPLICANT: Koulu, Markku  
; APPLICANT: Karvonen, Matti  
; APPLICANT: Pesonen, Ullamari  
; APPLICANT: Uusitupa, Matti  
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant  
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.  
; STREET: 555 13th Street NW, Suite 701-E  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/994,946A  
; FILING DATE: 19-DEC-1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihmen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 2328-110  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 551 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: mRNA  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 87..170  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 87..377  
; US-08-994-946A-5

Query Match 98.8%; Score 136.4; DB 3; Length 551;  
Best Local Similarity 99.3%; Pred. No. 3.8e-31;  
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCGC 60  
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCGC 60  
  
QY 61 CCAGCCACGCCCGCGCCGAGCCATCTAGGTAAACAGCGACCGGGGCTGTCCGGAC 120  
Db 61 CCAGCCACGCCCGCGCCGAGCCATCTAGGTAAACAGCGACCGGGGCTGTCCGGAC 120  
  
QY 121 TGACCCCTGCCCTGTCCC 138  
Db 121 TGACCCCTGCCCTGTCCC 138

RESULT 3  
US-09-291-994-5  
; Sequence 5, Application US/09291994  
; Patent No. 6312898  
; GENERAL INFORMATION:  
; APPLICANT: Koulu, Markku  
; APPLICANT: Karvonen, Matti

; APPLICANT: Pesonen, Ullamari  
; APPLICANT: Uusitupa, Matti  
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing  
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine  
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide  
; TITLE OF INVENTION: Y Gene.  
; FILE REFERENCE: 2328-112.A  
; CURRENT APPLICATION NUMBER: US/09/291,994  
; CURRENT FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (87)..(377)  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (87)..(170)  
; US-09-291-994-5

Query Match 98.8%; Score 136.4; DB 4; Length 551;  
Best Local Similarity 99.3%; Pred. No. 3.8e-31;  
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCGC 60  
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCGC 60  
  
QY 61 CCAGCCACGCCCGCGCCGAGCCATCTAGGTAAACAGCGACCGGGGCTGTCCGGAC 120  
Db 61 CCAGCCACGCCCGCGCCGAGCCATCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120  
  
QY 121 TGACCCCTGCCCTGTCCC 138  
Db 121 TGACCCCTGCCCTGTCCC 138

RESULT 4  
US-09-621-976-8234  
; Sequence 8234, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 8234  
; LENGTH: 122  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-621-976-8234

Query Match 80.9%; Score 111.6; DB 4; Length 122;  
Best Local Similarity 93.4%; Pred. No. 5.3e-24;  
Matches 114; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCGC 60  
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCGC 60  
  
QY 61 CCAGCCACGCCCGCGCCGAGCCATCTAGGTAAACAGCGACCGGGGCTGTCCGGAC 120  
Db 61 CCAGCCACGCCCGCGCCGAGCCATCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120  
  
QY 121 TG 122

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Db      121 TG 122

; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
; FILE REFERENCE: 2328-112.A
; CURRENT APPLICATION NUMBER: US/09/291,994
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-291-994-1

Query Match      64.8%; Score 89.4; DB 4; Length 325;
Best Local Similarity 89.7%; Pred. No. 1.7e-17;
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCCCGCAGCATAGTACTTGGCGC 60
Db      210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCCCGCAGCATAGTACTTGGCGC 60
QY      61 CCAGCCACGCGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
Db      270 CCAGCCACGCGCCGCGCGCCAGCCACCGTGTAGTCTAGACCCCGTCTG 316

RESULT 7
US-08-994-946A-2
; Sequence 2, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,946A
; FILING DATE: 19-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-994-946A-1

Query Match      64.8%; Score 89.4; DB 3; Length 325;
Best Local Similarity 89.7%; Pred. No. 1.7e-17;
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCCCGCAGCATAGTACTTGGCGC 60
Db      210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCCCGCAGCATAGTACTTGGCGC 269
QY      61 CCAGCCACGCGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
Db      270 CCAGCCACGCGCCGCGCGCCAGCCACCGTGTAGTCTAGACCCCGTCTG 316

RESULT 6
US-09-291-994-1
; Sequence 1, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
```

Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 87 ATGCTAGTAAACAGCGACCGGGCTGTCGGAGTACGACCTCGCCCTGTCCC 138  
Db  
30 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACGACCTCGCCCTGTCCC 81

## RESULT 8

US-09-291-994-2

; Sequence 2, Application US/09291994

; Patent No. 6312898

; GENERAL INFORMATION:

; APPLICANT: Koulou, Markku

; APPLICANT: Karvonen, Matti

; APPLICANT: Pesonen, Ullamari

; APPLICANT: Uusitupa, Matti

; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing

; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine

; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide

; TITLE OF INVENTION: Y Gene.

; FILE REFERENCE: 2328-112.A

; CURRENT APPLICATION NUMBER: US/09/291,994

; CURRENT FILING DATE: 1999-04-15

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 2

; LENGTH: 247

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-291-994-2

Query Match 36.5%; Score 50.4; DB 4; Length 247;  
Best Local Similarity 98.1%; Pred. No. 3.7e-06;  
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 ATGCTAGTAAACAGCGACCGGGCTGTCGGAGTACGACCTCGCCCTGTCCC 138

Db 30 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACGACCTCGCCCTGTCCC 81

## RESULT 9

US-09-252-991A-14797/c

; Sequence 14797, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 14797

; LENGTH: 945

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-14797

Query Match 23.3%; Score 32.2; DB 4; Length 945;  
Best Local Similarity 52.6%; Pred. No. 0.84;  
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTGCGCGC 60

Db 611 ACCCCGCGGGTGGCAACCGAGACGTTGACATCGCCCGCTGCCCTGCCCGCAGCATC 552

QY 61 CCAGCCAGCGCGCGCGACCGACCATCATCTAGGTAAACAAGCGACCGGGGTGTCCGGAC 120

Db 551 CCCGCGACGCGCTCGCGCAACACCAAGGTGGGACGAGCAACGCGGAGCTCGGCC 492

QY 121 TGACCCCTCGCCCT 133

Db 491 TCAATCTCGTCT 479

## RESULT 10

US-09-252-991A-14954

; Sequence 14954, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 14954

; LENGTH: 2550

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-14954

Query Match 23.3%; Score 32.2; DB 4; Length 2550;  
Best Local Similarity 52.6%; Pred. No. 0.94;  
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTGCGCGC 60

Db 1880 ACCCGCGGGTGGCAACCGAGACGTTGACATCGCCCGCTGCCCTGCCCGCAGCATC 1939

QY 61 CCAGCCAGCGCGCGCGCGCCAGCCACCATCTAGGTAAACAAGCGACCGGGGTGTCCGGAC 120

Db 1940 CCCGCGACGCGCGCTCGGCAACACCAAGGTGGGACGAGCAACGCGGAGCTCGGCC 1999

QY 121 TGACCCCTCGCCCT 133

Db 2000 TCAATCTCGTCT 2012

## RESULT 11

US-09-252-991A-9668/c

; Sequence 9668, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 9668

; LENGTH: 1242

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9668

Query Match 23.0%; Score 31.8; DB 4; Length 1242;  
Best Local Similarity 54.8%; Pred. No. 1.1;  
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 24 CTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGCCCGACCGCGCGCGCGCCAGCC 83



Db 947 CTCGAAGACCGCCGACAGACCGCTCTCGATATGGCCACGCGCGCCAGCTTCCTGGCC 888  
QY 84 ACCATGCTAGGTAAACAGCGACCGGGCTGTCCGAGCTGACCTCGCCCTGTGCC 138  
Db 887 AACATGAGCACGAGATCCGACGCGCTGAACGGCTGTCTGGCATGCTCTCGC 833

## RESULT 12

US-09-252-991A-9746/c  
; Sequence 9746, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9746  
; LENGTH: 1521  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9746

Query Match 23.0%; Score 31.8; DB 4; Length 1521;  
Best Local Similarity 54.8%; Pred. No. 1.2;  
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;  
QY 24 CTCGGAGAGCTCGCCCGACAGCATAGTACTTCCGCCACGACCGCCGCGCCAGCC 83  
Db 1506 CTCGAAGACCGCCGACAGACCGCTCTCGATATGGCCACGCGCGCCAGCTTCCTGGCC 1447  
QY 84 ACCATGCTAGGTAAACAGCGACCGGGCTGTCCGAGCTGACCTCGCCCTGTGCC 138  
Db 1446 AACATGAGCACGAGATCCGACGCGCTGAACGGCTGTCTGGCATGCTCTCGC 1392

## RESULT 13

US-09-252-991A-9494  
; Sequence 9494, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9494  
; LENGTH: 2511  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9494

Query Match 23.0%; Score 31.8; DB 4; Length 2511;  
Best Local Similarity 54.8%; Pred. No. 1.2;  
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;  
QY 24 CTCGGAGAGCTCGCCCGACAGCATAGTACTTCCGCCACGACCGCCGCGCCAGCC 83  
Db 932 CTCGAAGACCGCCGACAGACCGCTCTCGATATGGCCACGCGCGCCAGCTTCCTGGCC 991  
QY 84 ACCATGCTAGGTAAACAGCGACCGGGCTGTCCGAGCTGACCTTCGCCCTGTGCC 138

Db 992 AACATGAGCACGAGATCCGACGCGCTGAACGGCTGTCTGGCATGCTCTCGC 1046

## RESULT 14

US-09-252-991A-9541  
; Sequence 9541, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9541  
; LENGTH: 2583  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9541

Query Match 23.0%; Score 31.8; DB 4; Length 2583;  
Best Local Similarity 54.8%; Pred. No. 1.2;  
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;  
QY 24 CTCGGAGAGCTCGCCCGACAGCATAGTACTTCCGCCACGACCGCCGCGCCAGCC 83  
Db 1096 CTCGAAGACCGCCGACAGACCGCTCTCGATATGGCCACGCGCGCCAGCTTCCTGGCC 1155  
QY 84 ACCATGCTAGGTAAACAGCGACCGGGCTGTCCGAGCTGACCTTCGCCCTGTGCC 138  
Db 1156 AACATGAGCACGAGATCCGACGCGCTGAACGGCTGTCTGGCATGCTCTCGC 1210

## RESULT 15

US-09-252-991A-14871  
; Sequence 14871, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14871  
; LENGTH: 999  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14871

Query Match 22.6%; Score 31.2; DB 4; Length 999;  
Best Local Similarity 52.3%; Pred. No. 1.7;  
Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
QY 7 TCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCCGACAGCATAGTACTTCGCCGCCAGCC 66  
Db 493 TCGCCCGACCGCGCACCTCTCTGTTCCCGGACGAACCTGCACGTTTCCGCGACGCTGGCC 552  
QY 67 ACCCGCCGCGCCGACGACCATCTAGGTAAACAGCGACCGGGCTGTCCGGAGCTGACCC 126  
Db 553 AAGTGCTGGCCAGCAAGCTTCGAAGTCACTTTCAACCGTGACTTCGGGGGGTGATC 612

Qy 127 TCGCCCTGTGCC 138  
| | | | |  
Db 613 CAGGCTTGTGCC 624

Search completed: April 26, 2004, 15:48:02  
Job time : 60.5 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:26 ; Search time 245 Seconds  
(without alignments)

2539.553 Million cell updates/sec

Title: US-09-645-590-2

Perfect score: 138

Sequence: 1 accccatcgctggctctca.....actgacctcgccctgtccc 138

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136.4	98.8	551	9	US-09-969-708-592
2	136.4	98.8	551	13	US-10-069-129-5
3	136.4	98.8	551	14	US-10-002-048A-1
4	136.4	98.8	551	15	US-10-236-903-5
5	136.4	98.8	551	15	US-10-017-273A-1
6	136.4	98.8	551	16	US-10-191-997-94
7	123.2	89.3	969	15	US-10-036-542-16
8	109.4	79.3	553	15	US-10-036-542-41
9	109.4	79.3	599	9	US-09-925-300-100
10	109.4	79.3	599	15	US-10-036-542-42
11	89.4	64.8	325	13	US-10-069-129-1
12	89.4	64.8	325	14	US-10-002-048A-3
13	89.4	64.8	325	15	US-10-236-903-1
14	89.4	64.8	646	13	US-10-027-632-127333

c	15	89.4	64.8	646	16	US-10-027-632-127333	Sequence 127333,
	16	87.8	63.6	496	10	US-09-918-995-2739	Sequence 2739, App
	17	61.2	44.3	417	15	US-10-205-823-288	Sequence 288, App
	18	51	37.0	1021	16	US-10-321-039-55	Sequence 55, Appl
	19	50.4	36.5	247	13	US-10-069-129-2	Sequence 2, Appl
	20	50.4	36.5	247	14	US-10-002-048A-4	Sequence 4, Appl
	21	50.4	36.5	247	15	US-10-236-903-2	Sequence 2, Appl
c	22	33.4	24.2	2175	13	US-10-425-114-33220	Sequence 33220, A
c	23	32.8	23.8	440	15	US-10-184-644-202	Sequence 202, App
c	24	32.8	23.8	440	15	US-10-063-685-52	Sequence 52, Appl
c	25	32.8	23.8	440	15	US-10-063-685-52	Sequence 52, Appl
	26	32.8	23.8	1020	15	US-10-156-761-7175	Sequence 7175, App
	27	32.8	23.8	9025608	15	US-10-156-761-1	Sequence 1, Appl
	28	32.4	23.5	2573	16	US-10-108-260A-672	Sequence 672, App
c	29	32.4	23.5	32329	13	US-10-374-903A-1	Sequence 1, Appl
	30	31.6	22.9	7185	15	US-10-329-079-48	Sequence 48, Appl
	31	31.6	22.9	61944	15	US-10-329-079-34	Sequence 34, Appl
	32	31.4	22.8	444	15	US-10-066-543-1069	Sequence 1069, App
	33	31.4	22.8	1959	15	US-10-156-761-6093	Sequence 6093, App
	34	31.2	22.6	1483	16	US-10-369-493-38984	Sequence 38984, A
	35	31	22.5	1338	16	US-10-369-493-35102	Sequence 35102, A
c	36	31	22.5	1487	16	US-10-369-493-43101	Sequence 43101, A
c	37	30.8	22.3	229	15	US-10-102-524-636	Sequence 636, App
	38	30.8	22.3	378	9	US-09-864-761-23299	Sequence 23299, A
	39	30.8	22.3	421	9	US-09-922-217-921	Sequence 921, App
	40	30.8	22.3	421	9	US-09-833-263-921	Sequence 921, App
	41	30.8	22.3	421	14	US-10-025-380-921	Sequence 921, App
	42	30.8	22.3	524	9	US-09-864-761-7432	Sequence 7432, App
c	43	30.8	22.3	540	15	US-10-066-543-60	Sequence 60, Appl
	44	30.8	22.3	650	15	US-10-066-543-436	Sequence 436, App
c	45	30.8	22.3	1108	9	US-09-800-729-42	Sequence 42, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-969-708-592  
; Sequence 592, Application US/09969708  
; Patent No. US20020102532A1  
; GENERAL INFORMATION:  
; APPLICANT: Augustus, Meena  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; FILE OF INVENTION: Sets  
; FILE REFERENCE: 689290-70  
; CURRENT APPLICATION NUMBER: US/09/969,708  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: US/60/237,606  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: US/60/237,608  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: US/60/237,425  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 658  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 592  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: Homosapiens  
US-09-969-708-592

Query Match 98.8%; Score 136.4; DB 9; Length 551;  
Best Local Similarity 99.3%; Pred. No. 1.4e-34;  
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGAGTACTGTCGCGC	60
Db	1	ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGAGTACTGTCGCGC	60
Qy	61	CCAGCCAGCCCGCGCGCCGACCATGCTAGTAAACAGCCGCGGCTCTCCGGAC	120
Db	61	CCAGCCAGCCCGCGCGCCGACCATGCTAGTAAACAGCCGCGGCTCTCCGGAC	120

QY 121 TGACCTCGCCCTGTCCC 138  
Db 121 TGACCTCGCCCTGTCCC 138

## RESULT 2

US-10-069-129-5  
; Sequence 5, Application US/10069129  
; Publication No. US20030224362A1  
; GENERAL INFORMATION:  
; APPLICANT: Jussi Kauhanen, Matti Karvonen, Ullamari Pesonen, Markku Koulou, Matti  
; APPLICANT: Uusitupa  
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing  
; TITLE OF INVENTION: Alcoholism Based on Leucine7 to Proline 7 Polymorphism in the P  
; TITLE OF INVENTION: Neuropeptide  
; TITLE OF INVENTION: Y Gene, and methods for the prevention and Treatment of Alcoholi  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/069,129  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (87)..(377)  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (87)..(170)  
US-10-069-129-5

Query Match 98.8%; Score 136.4; DB 13; Length 551;  
Best Local Similarity 99.3%; Pred. No. 1.4e-34;  
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
QY 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGGCTGTCCGGAC 120  
Db 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120  
QY 121 TGACCTCGCCCTGTCCC 138  
Db 121 TGACCTCGCCCTGTCCC 138

## RESULT 3

US-10-002-048A-1  
; Sequence 1, Application US/10002048A  
; Publication No. US20020182616A1  
; GENERAL INFORMATION:  
; APPLICANT: Wahlestedt, Claes  
; APPLICANT: Ding, Bo  
; TITLE OF INVENTION: Single Nucleotide Polymorphisms  
; FILE REFERENCE: 10806-143  
; CURRENT APPLICATION NUMBER: US/10/002,048A  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: SE 0004035-2  
; PRIOR FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (87)..(380)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (87)..(170)  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank/K01911  
; DATABASE ENTRY DATE: 1995-01-07  
US-10-002-048A-1

Query Match 98.8%; Score 136.4; DB 14; Length 551;  
Best Local Similarity 99.3%; Pred. No. 1.4e-34;  
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
QY 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGGCTGTCCGGAC 120  
Db 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120  
QY 121 TGACCTCGCCCTGTCCC 138  
Db 121 TGACCTCGCCCTGTCCC 138

## RESULT 4

US-10-236-903-5  
; Sequence 5, Application US/10236903  
; Publication No. US20030093821A1  
; GENERAL INFORMATION:  
; APPLICANT: Hormos Medical Oy, Ltd.  
; APPLICANT: Koulou, Markku  
; APPLICANT: Karvonen, Matti  
; APPLICANT: Pesonen, Ullamari  
; APPLICANT: Uusitupa, Matti  
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant Prepro-Neuropeptide Y, a Mutant  
; TITLE OF INVENTION: Peptide, and Uses Thereof  
; FILE REFERENCE: 2328-126  
; CURRENT APPLICATION NUMBER: US/10/236,903  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 09/472,188  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 08/994,946  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (87)..(377)  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (87)..(170)  
US-10-236-903-5

Query Match 98.8%; Score 136.4; DB 15; Length 551;  
Best Local Similarity 99.3%; Pred. No. 1.4e-34;  
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60  
QY 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGGCTGTCCGGAC 120  
Db 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120

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QY 121 TGACCCCTCGCCCTGTCC 138
Db 121 TGACCCCTCGCCCTGTCC 138

RESULT 5
US-10-017-273A-1
; Sequence 1, Application US/10017273A
; Publication No. US20030119714A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Naylor, Alasdair M.
; APPLICANT: Van Der Graaf, Pieter H
; APPLICANT: Wayman, Christopher P.
; TITLE OF INVENTION: Treatment of Male Sexual Dysfunction
; FILE REFERENCE: PC22013
; CURRENT APPLICATION NUMBER: US/10/017,273A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/265,358
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: GB 0030647.2
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: GB 0108730.3
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: GB 0120679.6
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 09/905,846
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/291,722
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 09/895,367
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-017-273A-1

Query Match 98.8%; Score 136.4; DB 15; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.4e-34;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTCGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCCATCCGCTCGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 60
QY 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCCGAC 120
Db 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCCGAC 120
QY 121 TGACCCCTCGCCCTGTCC 138
Db 121 TGACCCCTCGCCCTGTCC 138

RESULT 6
US-10-191-997-94
; Sequence 94, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: NPY: Acc. No. US20030207834A1 K01911
US-10-191-997-94

Query Match 98.8%; Score 136.4; DB 16; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.4e-34;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTCGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCCATCCGCTCGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 60
QY 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCCGAC 120
Db 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCCGAC 120
QY 121 TGACCCCTCGCCCTGTCC 138
Db 121 TGACCCCTCGCCCTGTCC 138

RESULT 7
US-10-036-542-16
; Sequence 16, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002p1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (118)..(118)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (254)..(255)
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; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (839)..(839)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (887)..(887)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (897)..(897)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-036-542-16

Query Match 89.3%; Score 123.2; DB 15; Length 969;  
Best Local Similarity 96.2%; Pred. No. 2.4e-30;  
Matches 125; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 9 CGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCAC 68  
||  
Db 250 CGAGNNCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCAC 309  
||  
Qy 69 GCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCGGGCTGTCCGGACTGACCCCTC 128  
||  
Db 310 GCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTC 369  
||  
Qy 129 GCCCTGTCCC 138  
||  
Db 370 GCCCTGTCCC 379  
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## RESULT 8

US-10-036-542-41  
; Sequence 41, Application US/10036542  
; Publication No. US20030083481A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.

; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins  
; FILE REFERENCE: PA002P1  
; CURRENT APPLICATION NUMBER: US/10/036,542  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: PCT/US00/19666  
; PRIOR FILING DATE: 2000-07-20  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 60/144,972  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/149,173  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/158,004  
; PRIOR FILING DATE: 1999-10-06  
; PRIOR APPLICATION NUMBER: 60/194,689  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 157  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 553  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-036-542-41

Query Match 79.3%; Score 109.4; DB 15; Length 553;  
Best Local Similarity 98.4%; Pred. No. 6.9e-26;  
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 16 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCACGCCGCG 75  
1 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCACGCCGCG 60  
Db 76 GCCAGCCACCATGTAGGTAAACAGCGACCGGGCTGTCCGGACTGACCCCTGCGCCCTGT 135  
61 GCCAGCCACCATGTAGGTAAACAGCGACTGGGGCTGTCCGGACTGA-CCTCGGCCCTGT 119  
Qy 136 CCC 138  
||

Db 120 CCC 122

## RESULT 9

US-09-925-300-100  
; Sequence 100, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 100  
; LENGTH: 599  
; TYPE: DNA

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (583)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (584)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (599)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-100

Query Match 79.3%; Score 109.4; DB 9; Length 599;  
Best Local Similarity 98.4%; Pred. No. 6.9e-26;  
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 16 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCACGCCGCG 75  
||  
Db 14 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCGCCAGCCACGCCGCG 73  
||  
Qy 76 GCCAGCCACCATGTAGGTAAACAGCGACCGGGCTGTCCGGACTGACCCCTGCGCCCTGT 135  
||  
Db 74 GCCCA-CCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTGCGCCCTGT 132  
||  
Qy 136 CCC 138  
||  
Db 133 CCC 135  
||

## RESULT 10

US-10-036-542-42  
; Sequence 42, Application US/10036542  
; Publication No. US20030083481A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.

; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins  
; FILE REFERENCE: PA002P1  
; CURRENT APPLICATION NUMBER: US/10/036,542  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: PCT/US00/19666  
; PRIOR FILING DATE: 2000-07-20  
; PRIOR APPLICATION NUMBER: 60/144,972  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 60/148,681  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/149,173  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/158,004  
; PRIOR FILING DATE: 1999-10-06

; PRIOR APPLICATION NUMBER: 60/194,689  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 157  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (583)..(584)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (599)..(599)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-036-542-42

Query Match 79.3%; Score 109.4; DB 15; Length 599;  
Best Local Similarity 98.4%; Pred. No. 6.9e-26;  
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 16 TCTACCCCTCGGAGAGCGCTCGCCGACGACATAGTACTTGGCGCCCGACGCGCCGCG 75  
Db 14 TCTACCCCTCGGAGAGCGCTCGCCGACGACATAGTACTTGGCGCCCGACGCGCCGCG 73  
QY 76 CGCCAGCCACCATGCTAGGTAAAGAGCGCGGGCTGTCCGACTGACCTCGCCCTGT 135  
Db 74 CGCCA-CCACCATGCTAGGTAAAGAGCGACTGGGCTGTCCGACTGACCTCGCCCTGT 132  
QY 136 CCC 138  
Db 133 CCC 135

RESULT 11  
US-10-069-129-1  
; Sequence 1, Application US/10069129  
; Publication No. US2003024362A1  
; GENERAL INFORMATION:  
; APPLICANT: Jussi Kauhanen, Matti Karvonen, Ullamari Pesonen, Markku Koulou, Matti  
; APPLICANT: Uusitupa  
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing  
; TITLE OF INVENTION: Alcoholism Based on Leucine7 to Proline 7 Polymorphism in the Pr  
; TITLE OF INVENTION: Neuropeptide  
; TITLE OF INVENTION: Y Gene, and methods for the prevention and Treatment of Alcoholi  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/069,129  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-069-129-1

Query Match 64.8%; Score 89.4; DB 13; Length 325;  
Best Local Similarity 89.7%; Pred. No. 2e-19;  
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 60  
Db 210 ACCCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 269  
QY 61 CCAGCCACGCGCGCGCCGACCATGCTAGTAAACAGCGACCG 107  
Db 270 CCAGCCACGCGCGCGCCGACCATGCTAGTAAACAGCGACCG 316  
RESULT 12  
US-10-002-048A-3

; Sequence 3, Application US/10002048A  
; Publication No. US20020182616A1  
; GENERAL INFORMATION:  
; APPLICANT: Wahlestedt, Claes  
; APPLICANT: Ding, Bo  
; TITLE OF INVENTION: Single Nucleotide Polymorphisms  
; FILE REFERENCE: 10806-143  
; CURRENT APPLICATION NUMBER: US/10/002,048A  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: SE 0004035-2  
; PRIOR FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: prim transcript  
; LOCATION: (210)..(325)  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank/M14295  
; DATABASE ENTRY DATE: 1995-01-08  
US-10-002-048A-3

Query Match 64.8%; Score 89.4; DB 14; Length 325;  
Best Local Similarity 89.7%; Pred. No. 2e-19;  
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 60  
Db 210 ACCCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 269  
QY 61 CCAGCCACGCGCGCGCCGACCATGCTAGTAAACAGCGACCG 107  
Db 270 CCAGCCACGCGCGCGCCGACCATGCTAGTAAACAGCGACCG 316

RESULT 13  
US-10-236-903-1  
; Sequence 1, Application US/10236903  
; Publication No. US20030093821A1  
; GENERAL INFORMATION:  
; APPLICANT: Hormos Medical Oy, Ltd.  
; APPLICANT: Koulou, Markku  
; APPLICANT: Pesonen, Ullamari  
; APPLICANT: Uusitupa, Matti  
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant Prepro-Neuropeptide Y, a Mutant  
; TITLE OF INVENTION: Peptide, and Uses Thereof  
; FILE REFERENCE: 2328-126  
; CURRENT APPLICATION NUMBER: US/10/236,903  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 09/472,188  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 08/994,946  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-236-903-1

Query Match 64.8%; Score 89.4; DB 15; Length 325;  
Best Local Similarity 89.7%; Pred. No. 2e-19;  
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 60  
Db 210 ACCCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 269

